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OM nucleic - nucleic search, using sw model

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July 9, 2004, 18:07:37 ; Search time 4046 Seconds (without alignments) 16047.421 Million cell updates/sec
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                                                                                              3470272 seqs, 21671516995 residues
                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			o			SUMMARIES	
	Result No.	Score	% Query Match	Leng	DB	ΠD	scriptio
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	REFERENCE		(base	s 1 to	1396)		
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Simmondsiaceae; Simmondsia.
1 (bases 1 to 1702)
Lassner, M.W., Emig, R.A., Ruezinsky, D.M. and Benennaam, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 GGCTGGGCTGGGCTGGGCTGGGCATGGCTATTGCAGCAGCAGCGCGTGGTGGTACC 157
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MICHAEL W LASSNER, ROBIN A EMIG, DIANE M RUEZINSKY, ALISON VAN BENENNAAM
CI2N15/09, A01H5/00, C12N5/10//C12N9/10, C12N15/00, C12N5/00 CC
             840 AGACTCTTCAAGGGACAACCTTCAGTGGTGCATGTTCATATCAAGAGGCATTTGATGAAG
                                                                                                                                                       AGACTOTTTGAGGGGGGGACCTTCTGTGGTGCATGTGCACATCAAGAGGCATGTAATGAGG
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Patent: JP 2002525105-A 142 13-AUG-2002;
CALGENE LLC
OS Simmondsia chinensis
PN JP 2002525105-A/142
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572337
PR 25-SEP-1999 US 60/101939
PI MICHAEL W LASSNER, ROBIN A EMIG, DIANE P EDRINAAM
PC C12N15/09, A01H5/00, C12N5/10//C12N9/10, unsure at all n locations
FH Key
Location (1702).
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Location/Qualifiers
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Identification of differentially expressed genes during dehydration in almond (Prunus amygdalus) using the cDNA-AFLP technique Unpublished

2 (bases 1 to 1396)
Campalans, A., Pages, M. and Messeguer, R.
Direct Submission
Submitted (10-DEC-1999) Genetica Molecular, Centre d'Investigacio i Desenvolupament (CSIC), C/Jordi Girona, 18-26, Barcelona 08034,
                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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SQSERSTPAPVAPTNNKNKGESSGKPEKQQ"
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185. .1105
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BURATYOLA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Brassicacee; Arabidopsis.

ELASTICA. BENESTRA. A., Ruezinsky, D. M. and Eenennaam, A. V.
Novel plant acyltransferases
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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.

Full-length messenger RNA sequences greatly improve genome
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Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs
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Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R.
Feldmann, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lu, Y.-P., Flavell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lichary (1980)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Feldmann, K.
Full-Length cDNA from Arabidopsis thaliana
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available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the certain polymorphisms when compared to sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the coances, selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein id="AAM61033.1"
/db_xref="G1:21536701"
/translation="MV1AAAVIVPLGLLFFISGLAVNLFQAVCYVLIRPLSKNTYRKINTranslation="MV1AAAVIVPLGLLFFISGLAVNLFQAVCYVLIRPLSKNTYRKINTVAETLWLELVWIVDWWAGVKIQVFADNETFNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSEYLFLERNWAKDESTLKSGLQRLSDFPRPFWLALFVEGTRFTEAKLKAQEYAASSELPIPRNVLIPRTKSFVSAVSNMRSFVPAIYDMTVTIPKTSPPPTMLRLFKGQPSVVHVHIKCHSMKDLPESDDAIAQWCRDQFVAKDALDKHIAADTFPGQQEQNIGRPIKSLAVVLSWACVLTLGAIKFLHWAQLFSSWKGITISALGLGIITLCMQILRSSQSERSTPAKVVPAKPKNNHHPESSSQTETEKEK"
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/product="1-acylcerol-3-phosphate acyltransferase-like
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Best Local Similarity 74.1%; Pred. No. 2e-150;
Matches 824; Conservative 0; Mismatches 288;
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="108727"
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DNA SEQUENCE ENCODING PLANT 2-ACYLTRANSFERASE
Patent: WO 9624674-A 3 15-AUG-1996;
GENE SHEARS PTY LTD (AU)
Other publication AU 4669096 960827.
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Pred. No. 3.9e-148;
0; Mismatches 298;
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LDAGPATMR 17-NOV-1995
L.douglasii mRNA for 1-acyl-sn-glycerol-3-phosphate acyltransferase (putative).
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Z48730.1 GI:1067137
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Limnanthes douglasii (Douglas's meadowfoam)
Limnanthes douglasii (Douglas's meadowfoam)
Limnanthes douglasii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Limnanthaceae; Limnanthes.
1 (bases 1 to 1486)
Brown, A.P., Brough, C.L., Kroon, J.T. and Slabas, A.R.
Identification of a cDNA that encodes a
1-acyl-sn-glycerol-3-phosphate acyltransferase from Limnanthes
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Brown, A.P., Brough, Cl., Kroon, J.T. and Slabas, A.R. Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-phosphate acyltransferase from
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Slabas,A.R., Brown,A.P., Brough,C.L. and Kroon,J.T.M.
DNA sequence encoding plant 2-acyltransferase
Patent: US 6583340-A 3 24-JUN-2003;
Location/Qualifiers
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Pred. No. 3.9e-148;
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University of Durham, Science Laboratories, Durham, County Durham,
DH1 3LE, UK
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988 AATTTATATCCAAGGATGCATTGTTAGACAAACATGTTGCTGAGGATACTTTCAGTGGCC
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Slabas, A.R. and Brown, A.P.
DNA ENCODING 2-ACYLTRANSFERASES
Patent: WO 9413814-A 1 23-JUN-1994;
NICKERSON BIOCEM LTD (GB)
Other publication SK 76395 950913
Other publication AU 5656794 940704
Other publication AU 71785 960228
Other publication HU 71785 960228
Other publication FL 309327 951002.
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Sequence 1 from Patent WO9413814.
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/db_xref="taxon:32644"
130_.1254
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Db 1065 GTGCCTCCTGCTG Qy 1124 GAAGGGTGTTGCA	Db 1125 GAGGGGTGTGGCG Qy 1184 GATTCAATTCTCA	118	RESULT 10 AR062686 LOCUS AR062686	AR062686 AR062686.1	-	AUINCKS SIADAS, A.KYSZAL TITLE DNA encoding 2- JOURNAL Patent: US 5843 FEATURES LOCATI	5	Query Match Best Local Similarity 6 Matches 770; Conservati	104 GCTGGGCTG 	Qy 164 CCIGCICTICTIC             Db 168 CCIGCICTICCIC	Qy 224 CGTAAGGCCGGTG           Db 228 GATAAGGCCCTTT	Qy 284 GTGGCTGGAGCTT               Db 288 GTGGCTTCAGCTT	OY 344 AGATCATGAAACC 	Oy 404 AAGTGATATTGA1	Oy 464 CACTCTAGCTGT(	Oy 524 GTTTCTGAGTA'              	4 0 0	OY 644 AACGCGTTTAC	
VAFTAAGMALVTGVMHVFIMFSQAERSSSARAARNRVKKE"	Query Match 36.6%; Score 548.8; DB 6; Length 1514; Best Local Similarity 68.8%; Pred. No. 5.5e-125; Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;	104 GCTGGGCTGGGCTGGGCTATTGCAGCGGCCGTGGTGGTACCATTGGG 163	164 CCTGCTCTTCGCCTCCGGCCTCCTTGTTAATCTCAGGCAATATGCTATGTCGT 223	224 CGTAAGGCCGGTGTCGAAAAGTTTGTACAGAAGGATCAACCGGGTAGTAGCAGAGCTCTT 283	8 8 8 8	344 AGATCATGAAACCTTTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAG 403 	404 AAGTGATATTGATTGGCTTGTTGGATGGGTTTCAGCTCCAGCGTTCAGGTTGTCTTGGCAG 463	464 CACTCTAGCTGTGATGAAGAATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTCAATGTG 523	GTTTTCTGAGTACTTTTTCTGGAGAAGTTGGCCAAGGATGAAAGCACATTAAAGTC 58	4, 00	4 8	704 GCCTGTTCCTAGAATGTTTTGATTCCAAGAACTAAGGGTTTTGTTTCTGCAGTAAGTCA 763	764 TATGCGCTCATTTGTTCCTGCCATTTATGATGTAACAGTAGCCATCCCTAAGAGTTCCCC 823	824 IGCTCCTACAATGCTAAGACTCTTCAAGGACAACCTTCAGTGGTGCATGTTCATATCAA 883	4 00	944 TATATTTGTGGCCAAGGAIGCTTTGTTAGACAAACATATGGCTGAGGGTACTTTAGTGA 1003	4 TCAAGAGCTGCAGGATACTGGTCGACCAATAAAGTCTCTTGTGGTAGTTATATCTTGGGC 106	1005 TGAGGAGATTAGACCTATTGGCCGTCCAGTGAATCATTGCTGGTGACCCTGTTCTGGTC 1064 1064 GTGTCTGGTTGTTGCGGGGTCTGTAAAGTTCCTGCAATGGTCTTCGTTACTCTTCCTG 1123	
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zard. and Brown, A. Paul.
2-acyltransferases
843739-A 1 01-DEC-1998;
ation/Qualifiers
.1514
Janism="unknown"
\_\_type="unassigned DNA" 1514 bp om patent US 5843739. :5990377

343

347 403 407 463 467 523 527 643

647 703 707 763 767 823 827 883 887 943 947

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ZM1AG3PAT 1518 bp mRNA linear PLN 17-NOV-1994 Z.mays (Black Mexican Sweet) mRNA for 1-acyl-glycerol-3-phosphate acyltransferase (putative). Z29518
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Pred. No. 5.5e-125;
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Unclassified.

1 (bases 1 to 1514)

Slabas, A. Ryszard. and Brown, A. Paul.
Plant expressing 2-acyltransferase
AL Patent: US 6194640-A 1 27-FEB-2001;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 1 from patent US 6194640.
AR135355 GI:14124260
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68.8%;
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1003

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lorganism="Zea mays"

/ organism="Zea mays"

/ organism="Zea mays"

/ strain="Black Mexican Sweet"

/ db xref="taxon:4577"

/ clone="pwd71"

/ tissue type="endosperm"

/ clone lib="puC13 Maize endosperm polyA+ library"

/ dev stage="endosperm, postpollination"

/ l33. .1257

/ codon_start=1

/ product="1-acyl-glycerol-3-phosphate acyltransferase

/ putative)"

/ protein_id="CAA82638.1"

/ db xref="GOA:Q41745"

/ db xref="GDA:Q41745"

/ db xref="SPTREMBL:Q41745"

/ db xref="SP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown, A.P.
Direct Submission
Submitted (18-JAN-1994) Adrian P Brown, Biological Sciences,
University of Durham, South, Road, Durham, County Durham, DH1 3LE,
U.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIGGCTTCAGCTTGTCTGGGGGACTGGACTGGTGGCAGGTGTTAAAGTACAACTGCATGC
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Pred. No. 5.5e-125;
0; Mismatches 347; Indels 3;
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1415 bp mRNA linear PLN 20-JUN-2003 wlkl.pk0004.e7:fis, full insert mRNA
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Triticum aestivum
Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1415)
Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
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                    GAGTGATATTGATTGGCTCATTGGATGGATATTGGCCCCAGCGTTCAGGGTGCCTTGGAAG
                                                            CACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTCAATGTG
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Triticum aestivum clone wl sequence.
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135. . 1070
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B.napus mRNA for 1-acyl-sn-glycerol-3-phosphate acyltransferase.
Z49860
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                                                                                                                                                                                                                                                                                                      1035 ATCCICITIGCITCIGGATIGGCARIGGIAACCGCGTTATGCATGTATTCATCATGTTC 1094
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1 (bases 1 to 1367)
Brown,A.P., Brough,Cl., Kroon,J.T. and Slabas,A.R.
Nucleotide sequence of a cDNA for a putative 1-acyl
Sn-glycerol-3-phosphate acyltransferase from rape
Unpublished
2 (bases 1 to 1367)
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Laboratories, South Road, Durham,
           858 GCAAAGGACGCTTATTGGACAAACATATAGCAACTGGTACTTT---TGATGAGGAAATT
                                                                                                               915 ATACCAATTGGCCGTCCAGTGAATCTTTGATGGTGGTCCTGTCTTGGTCGTCCTCTC
                                                                                                                                                                   1074 GTTGCGGGGTCTGTAAAGTTCCTGCAATGGTCTTCGTTACTCCTCTTCCTGGAAGGGTGTT
                                                                                                                                                                                                               975 CTATATGGTGCTCATAGATTCTTACAGTGGACCCAGCTCTTGTCGACGTGGAAAGGAGTG
                                                                               1014 CAGGATACTGGTCGACCAATAAAGTCTTCTGGTAGTTATATCTTGGGCGTGTCTGGTT
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Brassica napus (rape)
Brassica napus
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135._.1070
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1. .1367
/organism="Brassica napus"
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Brough, Cl.

Direct Submission

Submitted (13-JUN-1995) Clare L.

University of Durham, Science, L.

DHI 31E, England
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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BNAGPATRF
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   Direct Submission
Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
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Pred. No. 4.3e-119;
0; Mismatches 355; Indels
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                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                           35.0%;
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9 TCAGAGGTCAGGTTGCCTAGGAAGCGCATTAGCTGTGATGAAGAAGTCTTCCAAATTTCT 268	O GCCGGTCATTGGCTGGTCATGTGGTTTTCTGAGTATCTTTTCTGGAGAGAAGTTGGGC 559	O CAAGGATGAAAGCACATTAAAGTCAGGCATCCAGCGACTGAGTGATTTCCCTCTTCCCTT 61	9 AAAGGATGAAAGCACTTTAAAGTCAGGTCTTCAACGCTTGAACGACTTCCCACGGCCTTT 38	O TIGGCIAGCICTITIGIAGAAGGAACGCGITITACACAGGCCAACTATIAGCIGCICA 679 	O GGAATATGCCACTTCCACTGGATTGCCTGTTCCTAGAAATGTTTTGATTCCAAGAACTAA 739 	0 GGGTTTTGTTTCTGCAGTAAGTCATATGCGCTCATTTGTTCCTGCCATTTATGATGTAAG 79	9 AGGATTTGTGTCAGCTGTTAGTAACATGCGTTCATTTGTGCCAGCCA	O AGTAGCCATCCCTAAGAGTTCCCCTGCTCCTACAATGCTAAGGCTCTTCAAGGGACAACC 859	O TICAGIGGIGCAIGITCAIAICAAGAGGCAITIGAIGAAGGAACIGCCAGAIACAGAIGA 919	GGCTGTTGCTCAATGGTGTCGAGATATATTTGTGGCCAAGGATGCTTTGTTAGACAAACA 97		O TATGGCTGAGGGTACTTTTAGTGATCAAGAGCTGCAGGATACTGGTCGACCAATAAAGTC 1039 	O TCTTCTGGTAGTTATATCTTGGGCGTGTCTGGTTGTTGCGGGGTCTGTAAAGTTCCTGCA 1099	O ATGGTCTTCGTTACTCTCTGGAAGGGTGTTGCATTTTCAGCTTTTGGTTTGGCAGT 1159	O TGTTACTGCACTTATGCAAATTCTGATTCAATTCTCACAGTCAGAGCGTTCAAACCCGGC 1219	0 CAAGATCGTGCTAGAAAAAAAAAAAAA 1249	SAAGTCGCTCCAGCCAAAGGACAA 1018	AF479037  Triticum aestivum 1-acyl-glycerol-3-phosphate acyltransferase mRNA, partial cds. AF479037  AF479037  AF479037.1 GI:32400848  Triticum aestivum (bread wheat)
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/mol type="mRNA" /cultivar="PH 82-2-2" /db xref="taxon:4565" /tissue type="seeds" <1. 714 /note="similar to Zea mays 1-acy1-glycerol-3-phosphate

acyltransferase"

CDS

2 (bases 1 to 714)
Li,J.R., Wang,F., Li,Q.Z. and Zhang,X.S.
Direct Submission
Submitted (29-JAN-2002) College of Life Science, Shandong
Agricultural University, Dai Zong Street 61, Taian, Shandong
271018, P.R. China

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

1. .714 /organism="Triticum aestivum"

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603 AACATATAGCAACTGGTCTTTTGA 626

Search completed: July 9, 2004, 21:00:24 Job time : 4051 secs

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9, 2004, 18:01:02; Search time 467 Seconds (without alignments) 13626.982 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aaa64200 Nucleotid	Aaa37472 DNA encod		Aac50510 Arabidops	Aac36124 Arabidops		0		Aaa64201 Nucleotid	Aac50517 Arabidops	Aaa64183 Nucleotid	Aac43080 Arabidops	Aac43788 Zea mays	Aaa64184 Nucleotid	Aac38209 Zea mays	Aaa64182 Nucleotid	Aaa37432 Maize acy	Aaa37433 Maize acy	Abl73513 Corn tass	Aaa37434 Maize acy		Aaa37436 Maize acy	Aaa51068 Human LPA
QI	AAA64200	AAA37472	AAA37342	AAC50510	AAC36124	AAT35205	AAQ68267	AAA64199	AAA64201	AAC50517	AAA64183	AAC43080	AAC43788	AAA64184	AAC38209	AAA64182	AAA37432	AAA37433	ABL73513	AAA37434	AAA37435	AAA37436	AAA51068
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% Query Match	100.0	44.9	43.6	43.6	43.5	42.6	36.7	36.7	35.0	34.8	34.2	32.8	29.9	15.2	14.1	12.9	12.7	10.0	10.0	7.6		8.6	
Score	1498	672.8	652.8	652.8	651.4	637.4	550.4	549.2	525	520.6	511.8	491	448	228	210.8	193.2	190.6	150	150	145	132	129.4	121.8
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## ALIGNMENTS

RESULT 1

New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal. The present sequence encodes a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. Location/Qualifiers
126. 1259
/\*tag= a
/product= "lysophosphatidic acid acetyltransferase
(LPAAT) isoenzyme" Lysophosphatidic acid acetyltransferase, LPAAT, transgenic plant, triacylglycerol; oil content; ss. Nucleotide sequence of a lysophosphatidic acid acetyltransferase. KG; Kinney AJ, Ripp (DUPO ) DU PONT DE NEMOURS & CO E I. Claim 39; Page 99; 102pp; English. Hitz WD, BP. 22-FEB-2000; 2000WO-US004526. 99US-0121119P. AAA64200 ID AAA64200 standard; DNA; 1498 (first entry) Cahoon RE, WPI; 2000-558300/51. P-PSDB; AAB08478. WO200049156-A2 20-DEC-2000 22-FEB-1999; 24-AUG-2000. Glycine max. Cahoon EB, AAA64200; 

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This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding jojoba acyltransferase LPAAT, SEQ ID NO:161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
165. .1331
/*tag= a
/product= "Jojoba lysophosphatidic acid
(LPAAT)"
/transl_except= (pos:282. .287, aa:Thr)
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The invention relates to nucleic acids encoding novel plant

acyltransferase-like proteins (AAA37343-A3745) which comprise one of 8

conserved acyltransferase motifs (AAY99474-Y99481). Acyltransferases

catalyse the transfer of acyl groups from a donor to a variety of

substrates such as glycerides, sterols, stanols and phosphatides. Such

enzymes play a key role in lipid synthesis, and thereby affect the

characteristics of the plant. For example, cold-hardened plants have

different lipid concentrations in the cell membrane compared to non
characteristics of the plant. For example, cold-hardened plants have

different lipid concentrations in the cell membrane of luid and the plant more

characteristics of for expressing acyltransferase-like proteins in

can be used as probes or for expressing acyltransferase-like proteins in

host cells e.g., for recombinant protein production. They may be

expressed in plant cells to alter the lipid composition of the plant

e.g., for the production of chill-resistant plants, or for altering the

composition of plant oils. The present sequence represents DNA encoding

composition and acyltransferase (LPAAT) Novel acyltransferase related proteins useful for altering fluidity in plant cells e.g. to induce chill tolerance. Van Ž Ž Example 5; Page 98; 126pp; English. Ruezinsky Emig RA, 2000-303447/26 (CALJ ) CALGENE LLC WPI; 2000-303447/ P-PSDB; AAY99482, Σ Lassner 

736

796

GGGATTGCCAGTTCCTAGAAATACTTTGATCCCTCGTACTAAGGGATTTGTTTAGCCGT

TGGATTGCCTGTTCCTAGAATGTTTTGATTCCAAGAACTAAGGGTTTTGTTTCTGCAGT

698 737

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Eenennaam

membrane

677 AGAAGGAACACGATTTACCCAAGCTAAACTTTTAGCAGCTCAAGAATATGCTACTTCAAT

Sequence 1702 BP; 435 A; 368 C; 383 G; 514 T; 0 U; 2 Other;

ö 196 217 256 316 337 376 397 436 457 496 517 556 577 616 637 676 AGAAGGAACGCGTTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCAC 697 277 GGCTGGGCTGGGCTGGGCTGGGCATGGCTATTGCAGCAGCGGCCGTGGTACC 157 ATTGGGCCTGCTCTTCTTCGCCTCCGGCCTCCTTGTTAATCTCATTCAGGCAATATGCTA AATGTGGTTTTCTGAGTATCTTTTCTGGAGAAGTTGGGCCAAGGATGAAAGCACATT 557 TATGTGGTTTTCTGAGTACCTTTTTCTTGAGAAGCTGGGCCAAGGATGAAGCACATT gerrascriscricricricricricricricricricricarcaacricarrascrar rerecresicescentricaagnniacaiacaagarinaacagarinaacagaga 338 ATTCACAGATCATGAAACCTTTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAA GITCACAGATCCTGATACCTITCGGCTAATGGGTAAAGAGCATGCACTTGTGATATCAAA gegaagecacretererereargaagaarcareaaagrirereeeggrearagrigere GCTCTTGTGGCTGGAGCTTGTATGGCTTATTGATTGGTGGGCAGGAGTTAAGGTCCAAAT TGGCAGCACTCTAGCTGTGATGAAATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTC AAAGTCAGGCATCCAGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTTTGT TGTCGTCGTAAGGCCGGGTGTCGAAAAGTTTGTACAGAAGGATCAACCGGGTAGTAGCAGA 398 TCACAGAAGTGATATTGATTGGCTTGTTGGATGGGTTTCAGCTCAGCGTTCAGGTTGTCT Gaps .; 0 Length 1702; Indels Query Match
Best Local Similarity 73.7%; Pred. No. 1.9e-165;
Matches 854; Conservative 0; Mismatches 304; 497 518 578 158 218 257 278 458 638 137 197 377 98 Db 엄 엄 원 Op  $\delta$ 셤 ∂ Op 8 QΩ  $\delta$ d  $\delta$ 8  $\delta$ ઠ ठे

1177 1237 1036 1057 1096 1117 916 937 976 766 856 877 977 TCGAGACATTCGTCGCAAAGGATGCACTCCTGGACAAGCATAATGTAGATGACACTTT 1037 CGGAGATGAGTATCTGCAGGACACTGGCCGGCCTTGAAATCTCTTTGTAGCAGTCTCT Location/Qualifiers 1. .1170 /\*tag= a /product= "Arabidopsis thaliana lysophosphatidic acid acyltransferase ATLPAAT1" 758 AAGTCATATGCGCTCATTTGTTCCTGCCATTTATGATGTAACAGTAGCCATCCCTAAGAG 1157 ATCATGGAAGGGGGTCGCCTTCTCAGCCGCATGCCTTGTGCTCGTCACCATTCTTATGCA 797 gadoccaraticorridoritoricocogiciariaridationaacogiogicoricorradano riedecarrearcreceredeaecrrieaaarrecraearecrecerecraete TICCTGGAAGGGTGTTGCATTTTCAGCTTTTGGTTTGGCAGTTGTTACTGCACTTATGCA AATTCTGATTCTCACAGTCAGAGCGTTCAAACCCGGCCAAGATCGTGCCTGCAAA 878 TATCAAGAGGCATTTGATGAAGGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTG 998 TAGTGATCAAGAGCTGCAGGATACTGGTCGACCAATAAAGTCTCTTCTGGTAGTTATATC rigascargiciosinstracassascristravastricciosaarastricaraciorio TCGAGATATATTTGTGGCCAAGGATGCTTTGTTAGACAAACATATGGCTGAGGGTACTTT TICCCCTGCTACAATGCTAAGACTCTTCAAGGGACAACCTTCAGTGGTGCATGTTCA Lysophosphatidic acid acyltransferase, ATLPAAT1; lipid synthesis; recombinant expression; membrane fluidity; cold resistance; cDNA encoding Arabidopsis thaliana acyltransferase ATLPAAT1 BP. GTCAAAAACAAGGGGTC 1255 GCCCAAGACATGGTATC 1294 AAA37342 standard; cDNA; 1170 99WO-US022231 98US-0101939P (first entry) transgenic plant; ss. Arabidopsis thaliana. 15-AUG-2000 25-SEP-1998; 24-SEP-1999; 06-APR-2000 818 1097 1118 1178 1238 1277 938 1058 AAA37342; के विक 성 음 ద 셤 ò ď ò g ઠે q 95 25 26  $\delta$  $\delta$ 셤

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 AAGGGTTTTGTTTCTGCAGTAAGTCATAIGCGCTCATTTGTTCCTGCCATTTATGAIGTA 797
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99US-0123548P.
99US-0125788P.
99US-0126264P.
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990S-0127462P.
990S-0128234P.
990S-0128714P.
99US-0129845P.
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                                                Van Eenennaam A;
                                                                                                                                                                Novel acyltransferase related proteins fluidity in plant cells e.g. to induce
                                                                                                                                                                                                                                  5; Page 74-75; 126pp; English.
                                              Ruezinsky DM,
                                            Emig RA,
                                                                                          2000-303447/26
(CALJ ) CALGENE LLC
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Best Local Simil
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P-PSDB; AAR99249.
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                                                                                                                                                        Length 1480;
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Pred. No. 7.3e-160;
0; Mismatches 288;
99US-0160814P.
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74.1%;
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26-0CT-1999;
28-0CT-1999;
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Matches 824;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA for 2-acyl:transferase of Limnanthes douglasii - used to
transform oilseed plants, partic. Brassica, maize, sunflower or soya, for
improved oil prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-Acyltransferase, oilseed, lipid engineering, vegetable oil; canola; rape, Brassica napus; Brassica campestris; Brassica juncea; Brassica rapa; maize; Zea mays; sunflower; Helianthus annuus; soybean; Glycine max; transgenic plant; trierucin; erucic acid; ss.
                                                                                                                                                                                             1087 CACATAGCTGCAGACACTTTCCCCGGTCAACAAGAACATGGACATTGGCCGTCCCATAAAG
                                                                                                                    CATATGGCTGAGGGTACTTTTAGTGATCAAGAGCTGCAGGATACTGGTCGACCAATAAAG
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Limnanthes clone 1 (AAT35205) was obtd, by heterologous screening of a Limnanthes douglasii seed cDNA library using a 600 bp NcoI/PstI fragment of a rape 2-acyltransferase (2AT) clone corresponding to the N-terminus of the rape protein. It encodes the protein given in AAR99249. Another isolated clone (AAT35204) codes for the Limnanthes 2AT (AAR99248) useful for improving the erucic acid content of transgenic plants \*\*\*\*\*\*\*\*\*

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Sequence 1515 BP; 372 A; 339 C; 325 G; 479 T; 0 U; 0 Other;

TATTIGIGGCCAAGGAIGCITIGITAGACAAACAIAIGGCIGAGGGIACITITAGIGAIC 1005 ö 645 765 885 GCCATTTGATGAAGGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTCGAGATA 945 221 225 281 285 341 345 401 405 461 465 521 525 581 582 641 701 705 761 821 TGCGCTCATTTGTTCCTGCCATTTATGATGATGTAACAGTAGCCATCCCTAAGAGTTCCCCTG 825 881 AACCTACAATGCTCAGACTGTTCAGGGGGAAATCTTCTGTGGTACACGTACACCTTAAGC 941 TGCGCTCATTIGIC COAGCTATCTATGACTTGACAGTCGCCATTCCTAAAACCACGAAC AATTTATATCCAAGGATGCATTGTTAGACAAACATGTTGCTGAGGATACTTTCAGTGGCC ATACTGAGTCTTTCCGTCTAATGCGTAAAGAACATGCACTCTTAATATGCAACCACAGAA TTTCGAATATCTCTTTCTCGAGGGAACTGGGCCAAAGATGAAAACACTTTAAAGTCAG crestricacsaaascaaaacriciasciscissasaaraiscascerersessasiaa CTGTTCCTAGAAATGTTTTGATTCCAAGAACTAAGGGTTTTGTTTCTGCAGTAAGTCATA cedrecerceaaarerreaarrececeraceaaeeeerrrerereaeeerraeea CTCCTACAATGCTAAAGACTCTTCAAGGGACAACCTTCAGTGGTGCATGTTCATATCAAGA rrcrrrrrrangeagecregicarencarrrerrencarencarencia GGCTGGAGCTTGTATGGTTGGTGGGCCAGGAGTTAAAGGTCCAAATATTCACAG GGCTAGAACTTGTATGGGTCATTGATTGGTGGGCCAGGCGTTAAGGTCCAATTATATACTG ATCATGAAACCTTTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAGAA GTGACATTGACTGGCTCATTGGATGGGTCCTAGCACAGGGGATGCGGCTGCCTCAGTTCTT CTCTAGCTGTGAAGAAATCTTCAAAGTTTTCTGCCGGTCATTGGCTGGTCAATGTGGT caaraccrerrargaagaagrearccaaarrrecceggraaragerregreargregr TITCTGAGTATCTTTTCTGGAGAGAAGTTGGGCCAAGGATGAAAGCACATTAAAGTCAG GCATCCAGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTTTTGTAGAAGGAA CGCGTTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGC TGGGCTGGGCTGGGCTTGGCTATTGCAGCAGCGGCCGTGGTGGTACCATTGGGCC raccccaacraaagcraccardaccarccracracadcrararcarcararaagra TGCTCTTCTTCGCCCTCCGGCCTCCTTGTTAATCTCATTCAGGCAATATGCTATGTCGTCG TAAGGCCGGTGTCGAAAAGTTTGTACAGAAGGATCAACCGGGTAGTAGCAGAGCTCTTGT Gaps . Length 1515; Indels Score 637.4; DB 2; Pred. No. 3.4e-156; 0; Mismatches 301; Query Match
Best Local Similarity 73.1%;
Matches 818; Conservative 0 462 582 642 702 99/ 822 826 882 886 942 526 586 706 762 106 162 166 222 226 346 402 406 522 646 282 286 342 466 S B S B S B S 8 8 강염 g 2 g  $\delta$ d  $\delta$ 8 9 ò Db  $\delta$ 중 유 g S dd

1125 1241 2-Acyltransferase; lipid; oilseed; Escherichia coli; transgenic plant; crop improvement; ds. regaagrecaegacarregregeceaagraagrererrergergerreregarer GTCTGGTTGTTGCGGGGTCTGTAAAGTTCCTGCAATGGTCTTCGTTACTCTTCCTGGA ecchacicrecuredescriensaarircireasissicascacirrarcereas AGGGTGTTGCATTTTTGGTTTGGCAGTTGTTACTGCACTTATGCAAATTCTGA Complementation studies using a maize cDNA library transferred into coli JC201 allowed the isolation of a plasmid encoding a 2-acyltransferase enzyme from maize. DNA encoding 2-acyltransferase ca used to produce transgenic plants having altered lipid contents. (Up on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.) a plant 2-acryl-transferase - used to produce plants decreased lipid levels and with a tailored lipid comp TTCAATTCTCACAGTCAGAGCGTTCAAACCCGGCCAAGA 1224 AAGAGCTGCAGGATACTGGTCGACCAATAAAGT Location/Qualifiers 130. .1254 /\*tag= a ВР Disclosure, Fig 1, 45pp; English standard; cDNA; 1514 92GB-00025845 93WO-GB002528 BIOCHEM Maize 2-acyltransferase. (revised) (first ent Brown AP; WPI; 1994-217888/26. P-PSDB; AAR59712. (NICK-) NICKERSON DNA encoding increased or 10-DEC-1993; 10-DEC-1992; WO9413814-A1 25-MAR-2003 26-JAN-1995 Slabas AR, 1062 1122 1182 1186 1242 AAQ68267 1006 1066 1126 Zea mays AAQ68267 Сþ ò  $\delta$ 8 g

163 GCTGGGCTGGGCTGGCCATGCTATTGCAGCAGCGGCCGTGGTACCATTGGG Gaps ω .. Score 550.4; DB 2; Length 1514; Pred. No. 2e-133; 0; Mismatches 346; Indels 3; Query Match 36.7%; Best Local Similarity 68.8%; Matches 771; Conservative ( 104

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C; 405 G; 396 T; 0 U; 0 Other;

Sequence 1514 BP; 340 A; 373

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Matches 771; (
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The present sequence encodes a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT, The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes
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(LPAAT) isoenzyme"
                                                                                                                                                                                                                                                                            Lysophosphatidic acid acetyltransferase, LPAAT, transgenic plant, triacylglycerol; oil content; ss.
                                                                                                                                                                                                            Nucleotide sequence of a lysophosphatidic acid acetyltransferase
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The present sequence encodes a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes
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                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal.
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(LPAAT) isoenzyme"
                                 Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant; triacylglycerol; oil content; ss.
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acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants
which encode LPAAT at higher or lower levels than normal.
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/product= "lysophosphatidic acid acetyltransferase
(LPAAT) isoenzyme"
/note= "no termination codon given"
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(LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found.
                                                                                                                                                                                                                                                                                                                                                         1168 CACTTATGCAAATTCTGATTCAATTCTCAGAGTCAGAGGGTTCAAACCCGGCCAAG 1223
                                                                                                                                                                                                                                                                                                                                                                                       1128 GGGTCATGCACGTCTTCGTCATGTTCTCCCAGGCTGAGCGATCGAGCTCAGCCAAG 1183
                       TGCATGTTCATATCAAGAGGCATTTGATGAAGGAACTGCCAGATACAGATGAGGCTGTTG
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22. .502
/*tag= a /*troduct= "lysophosphatidic acid acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant; triacylglycerol; oil content; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a lysophosphatidic acid acetyltransferase.
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This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes	**************************************
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                                 Zea mays DNA fragment SEQ ID NO: 20162.
                                                17-OCT-2000 (first entry)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 3, Appli	'n	ı,	ì	12	12	84	74	14	16	16	Sequence 1820, Ap	'n					Sequence 1, Appli	ednence		equence					Sequence 60, Appl		
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US-08-245-809-3	US-08-107-748-2	PCT-US92-01385-2	US-09-790-988-1	US-09-790-988-1	US-09-640-173-53	US-09-713-550-53	US-08-245-809-5	US-08-107-748-4	PCT-US92-01385-4	US-09-621-976-18743	US-09-621-976-2813	US-09-489-847-23	US-09-601-198-4	US-09-647-390-15	US-08-916-421B-1	US-10-204-708-2	US-09-346-408-3	
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### **ALIGNMENTS**

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COUNTRY: us

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,581B

FILING DATE: March 14, 1997

PRICH RAPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB96/00306

FILING DATE: 09-FEB-1996

APPLICATION NUMBER: GB 9502468.3

FILING DATE: 09-FEB-1995

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1515 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FFATURE:
US-08-818-581B-3

Sequence 3, Application US/08818581B

Fatent No. 6583340

GENERAL INFORMATION:

APPLICANT: SLABAS, Antoni Ryszard

APPLICANT: BROWN, Adrian Paul

APPLICANT: BROWGH, Clare Louise

APPLICANT: KROON, Johannes Theodorus Maria

TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT

TITLE OF INVENTION: 2-ACYLTRANSFERASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

TID: 1005
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; LOCATION: 182.,1316
US-08-818-5818-3
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Length 1515; Query Match 42.9%; Score 642.2; DB 4; Length 1 Best Local Similarity 73.4%; Pred. No. 5.9e-187; Matches 821; Conservative 0; Mismatches 298; Indels

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LENGTH: 1514 base pairs
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STRANDEDNESS: double
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Best Local Similarity
Matches 770; Conserv
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FEATURE:
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; LOCATION:
US-08-454-267-1
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STATE: DC
COUNTRY:
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ZIP: 20005-3934

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,267
FILING DATE: 08-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB93/02528
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: REBD, GRANT E.
REGISTRATION NUMBER: 0623.0310000/JAG/GER
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.)
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.6%; Score 548.8; DB 2; larity 68.8%; Pred. No. 3.1e-158; Conservative 0; Mismatches 347;
US-08-454-267-1; Sequence 1, Application US/08454267; Patent No. 5843739
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RESULT 3
US-08-941-319-1
; Sequence 1, Application US/08941319
; Patent No. 5945323
; GENERAL INFORMATION:
; APPLICANT: SLABAS, ANTONI R.
; APPLICANT: BROWN, ADRIAN P.
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934

223 287 347 403 463 523 583 587 643 647 348 AGAIGAGGAAACTIACAGAICAAIGGGIAAAGAGCAIGCACTCATCAIATCAAATCAICG 407 467 527 168 cerecretrecretrededecerendares de contrades de contractor de contrac 284 GIGGCIGGAGCIIGIAIGGCIIAIIGAIIGGIGGGCAGGAGIIAAGGICCAAAIAIICAC 343 228 GATAAGGCCCTTTTCGAAGAGCTTCTACCGTCGGATCAACAGATTCTTGGCCGAGCTGCT 528 GTTTGCAGAGTACCTCTTTTTGGAAAGGAGCTGGGCCAAGGATGAAAAGACACTAAAGTG 288 drodcincaccindicidedicatedacidendededededitaaggracaccard 344 AGATCATGAAACCITTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAG 404 AAGTGATATTGATTGGCTTGTTGGATGGGTTTCAGCTCAGCGTTCAGGTTGTCTTGGCAG CACTCTAGCTGTGATGAAGAATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTCAATGTG 468 TACACTIGCIGICALGAAGAGICAICCAAGIICCTICCAGIIATIGGCIGGICAAIGIG GITITICIGAGIAICITITICIGGAGAGAAGITIGGGCCAAGGATGAAAGCACATIAAAGTC 584 AGGCATCCAGCGACTGAGTGATTTCCCTCTTTCGCTAGCTCTCTTTGTAGAAGG 104 GCTGGGCTGGGCTGGGCATGCCTATTGCAGCAGCGGCCGTGGTGCTACCATTGGG dedecececececeseceandeseancecececencerececencencerecece 164 CCTGCTCCTTCGCCTCCGGCCTCCTTGAATCTCATTCAGGCAATATGCTATGTCGT 224 CGTAAGGCCGGTGTCGAAAGTTTGTACAGAAGGATCAACCGGGTAGTAGCAGAGCTCTT Gaps ., М Length 1514; Indels COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,319
FILING DATE:
CLASSIFICATION NUMBER: 08/454,267
FILING DATE: 08-JUN 1995
APPLICATION NUMBER: PCT/GB93/02528
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2500
TELEFAX: (202) 371-250
TELEFAX: (202) 371-250
TELEFAX: (202) 371-250
TELEFAX: (202) 371-250
TELEGOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: Query Match 36.6%; Score 548.8; DB 2; Best Local Similarity 68.8%; Pred. No. 3.1e-158; Matches 770; Conservative 0; Mismatches 347; 108 524  $\overset{\diamond}{\circ}$ qq 임  $\delta$ 

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1514 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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; LOCATION:
US-09-035-098-1
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                                                   648 TACTCGCTTTACTCCAGCAAAGCTTCTCGCAGCTCAGGAATATGCGGCCTCCCAGGGCTT 707
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APPLICANT: SLABAS, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,098
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REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09035098 Patent No. 6194640 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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635 625 695 685 755 745

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993 AGCTCAGIGGCTICATAAACIGIACCAGGAGAAGGACGCGCCCCAGGAGATATATAAATCA 1052
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US-09-970-989A-12
i Sequence 12, Application US/09970989A
j Patent No. 6670143
j GENERAL INFORMATION:
j APPLICANT: LEUNG, DAVID W.
j APPLICANT: ADOUREL, DANIEL
APPLICANT: HOLLENBACK, DAVID
j TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
j TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
j CURRENT FILING DATE: 109/215, 252
prior APPLICATION NUMBER: 09/215, 252
prior APPLICATION NUMBER: 09/215, 252
prior PILING DATE: 1998-12-18
prior FILING DATE: 1996-03-19
prior FILING DATE: 1996-03-19
string APPLICATION NUMBER: 08/618, 651
prior FILING DATE: 1996-03-19
string APPLICATION NUMBER: 08/618, 651
j RIGHT FILING DATE: 1996-03-19
string APPLICATION NUMBER: 08/618, 651
j RIGHT FILING DATE: 1996-03-19
string APPLICATION NUMBER: 08/618, 651
j RIGHT FILING DATE: 1996-03-19
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j RIGHT FILING DATE: 1996-03-19
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516 CTTCGGAGTGCTGGAGGTCCTCGCTAAGAAGGAGCTGCTCTACGTGCCCCT
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Best Local Similarity 46.9%; Pred. No. 6.5e-27;
Matches 415; Conservative 0; Mismatches 467;
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NAME/KEY: CDS

LOCATION: (184)..(1311)

US-09-970-989A-12
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ORGANISM: Homo sapiens
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Sequence 12, Application US/09215252

Patent No. 6300487.

GENERAL INFORMATION:

APPLICANT: ADOUREL, David W.

APPLICANT: HOLLENBACK, David

TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

FILE REFERENCE: 077319/0151

CURRENT APPLICATION NUMBER: US/09/215,252

CURRENT FILING DATE: 1996-12-18

PRIOR FILING DATE: 1996-12-18

PRIOR FILING DATE: 1996-03-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 1660

TYPE: DAMMARE: PATENTINE OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF S
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Pred. No. 6.5e-27;
0; Mismatches 467;
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; NAME/KEY: CDS
; LOCATION: (184)..(1311)
US-09-215-252-12
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RESULT 7
US-09-620-312D-841
; Sequence 841, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Chen, Rui-hong
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xhao, Qing A.
; APPLICANT: Xue, Aidong J.
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: POLYPEPTIGES
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 841
LENGTH: 1769
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Best Local Similarity 46.8%;
Matches 414; Conservative
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
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US-09-215-252-14

i Sequence 14, Application US/09215252

i Sequence 14, Application US/09215252

i Patent No. 6300487

i GENERAL INFORMATION:

APPLICANT: LEUNG, David W.

APPLICANT: HOLLENBACK, Daniel

APPLICANT: HOLLENBACK, David

ITILE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

ITILE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

CURRENT APPLICATION NUMBER: US/09/215,252

CURRENT APPLICATION NUMBER: US 08/618,651

PRIOR PILING DATE: 1996-03-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14

LENGTH: 1523

TYPE: DNA

ORGANISM: Homo sapiens

FRAUCT: (233)..(1174)

US-09-215-252-14

AGCTIGIAIGGCTIAITGGTGGGCAGGAGTTAAGGTCCAAATATTCACAGATCATG 351 CCACGGTAGAGCGCTTTGGGAAGGAGCACGCAGTCATCATCCTCAACCCACAACTTCGAGA 344 CTGTGATGAAGAATCTTCAAAGTTTCTGCCGGTCATTGCCTGAATGTGGTTTTTCTG 531 591 225 AACTGGTCATGCTGCTGGAGTGGTCGTCCTGCACGGAGTGTACACTGTTCACGGACCAGG 284 TIGATIGGCITGIIGGAIGGGIITCAGCICAGCGIICAGGIIGICIIGGCAGCACICIAG 471 AGTATCTTTTTCTGGAGAGAGATGGGCCAAGGATGAAAGCACATTAAAGTCAGGCATCC 352 AAACCTTTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAGAAGTGATA 3; Gaps Length 1523; Query Match 7.2%; Score 108.6; DB 4; Length Best Local Similarity 47.6%; Pred. No. 7e-23; Matches 352; Conservative 0; Mismatches 384; Indels 412 285 345 472 465 405 592 à dd  $\stackrel{>}{\circ}$ g à 8 8 d  $\delta$ g 8

TGGCCAAGGATGCTTTGTTAGACAACATATGGCTGAGGGTACTTTTAGTGATCAAGAGC 1011 831 891 821 644 771 704 892 TGATGAAGGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTCGAGATATATTTG 951 GGACAGTCGCAGCTGTCTATGATGTAACCCTGAACTTC---AGAGGAAACAAGAACCCGT 761 882 AGGAGAAGGACGCCTCCAGGAGATATATAATCAGAAGGCCATGTTTCCAGGGGAGCAGT 941 762 CCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGGGGGGACATGTGCGTGAGGAGATTTC 822 CTCTGGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACC TCACGGAGACCAAGCACCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCC CTAGAAATGTTTTGATTCCAAGAACTAAGGGTTTTTGTTTCTGCAGTAAGTCATATGCGCT TCAAGTACCACCTGCTGCCGCGCGCCAAGGGCTTCACCACCGCAGTCAAGTGCCTCCGGG CATTIGITICTICCECCATTIATGATGIAACAGIAGCCATCCCTAAGAGITCCCCTGCTCTA TTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCCTGTTC rradecciecceaaece 960 952 1012 Вb  $\delta$ g à

US-09-970-989A-14

Sequence 14, Application US/09970989A

Sequence 14, Application US/09970989A

Patent No. 6670143

GENERAL INFORMATION:

APPLICANT: HOLLENBACK, DAVID

APPLICANT: ADOUREL, DANIEL

APPLICANT: ADOUREL, DANIEL

TILLS OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

FILE REFERENCE: 077319/0275

CURRENT APPLICATION NUMBER: US/09/970, 989A

CURRENT FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-03-19

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14

LENGTH: 1523

TYPE: DNA

ORGANISM: Homo sapiens

FRATURE:

NAME/KEY: CDS

LOCATION: (233)..(1174)

US-09-970-989A-14

284 411 344 404 412 TIGATIGGCTIGTIGGATGGGTTTCAGCTCCAGGTTGTCTTGGCAGCACTCTAG 471 531 285 CCACGCTAGAGCGCTTTGGGAAGGAGCACCCAGTCATCCTCAACCACAACTTCGAGA AACTGGTCATGCTGCAGGAGGGTGGTCCTGCACGGAGTGTACACTGTTCACGGACCAGG 352 AAACCTTTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAGAAGTGATA rcaacircicreradandaaccarararaadacacircadaacrecradadacrecaada CTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTCAATGTGGTTTTTCTG 292 AGCTIGIATGGCTTATTGATTGGTGGCCAGGAGTTAAGGTCCAAATATTCACAGATCATG Query Match 7.2%; Score 108.6; DB 4; Length 1523; Best Local Similarity 47.6%; Pred. No. 7e-23; Matches 352; Conservative 0; Mismatches 384; Indels 3; 225 345 셤 8 P 8 d ò

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US-09-970-989A-16

Sequence 16, Application US/09970989A

Patent No. 6670143

GENERAL INFORMATION:

APPLICANT: LEUNG, DAVID W.

APPLICANT: ADOUREL, DAVIEL

APPLICANT: HOLLENBACK, DAVID

TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

FILE REFERENCE: 077319/0275

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/215,252

PRIOR PLLING DATE: 1998-12-18

PRIOR FILING DATE: 1996-03-19

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 16

LENGTH: 1774
GTCGTCGTAAGGCCGGTGTCGAAAAGTTTGTACAGAAGGATCAACCGGGTAGTAGCAGAG
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APPLICANT: LEUNG, David W.
APPLICANT: ADOUREL, Daniel
APPLICANT: HOLLENBACK, David
TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
FILE REFERENCE: 077319/0151
CURRENT APPLICATION NUMBER: US/09/215,252
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: US 08/618,651
PRIOR FILING DATE: 1996-03-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
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; LOCATION: (158)..(1291)
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Pred. No. 3e-20;
0; Mismatches 423;
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Best Local Similarity 47.0%;
Matches 380; Conservative
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (158)..(1291)
US-09-970-989A-16
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Sequence 1820, Application US/09833381 Patent No. 6672186 GENERAL INFORMATION:

RESULT 12 US-09-833-381-1820

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENE BUCCOLING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: JII-002CNCP

CURRENT APPLICATION NUMBER: US/08/213,419B

CURRENT FILING DATE: 1994-03-14

PRIOR APPLICATION NUMBER: US 07/870,506

PRIOR FILING DATE: 1992-04-17

NUMBER OF SEQ ID NOS: 20
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APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1820
LENGTH: 809
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                                                                                                                                                                                                                                                                                                                                Length 809;
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3.4%; Score 51.4; DB 4; Length 8
Best Local Similarity 47.9%; Pred. No. 1.8e-05;
Matches 148; Conservative 0; Mismatches 161; Indels
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LOCATION: (2407)..(2439)
NAME/KEY: CDS
LOCATION: (2598)..(3404)
NAME/KEY: CDS
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; NAME/KEY: CDS
; LOCATION: (3850)..(5835)
US-08-213-419B-3
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CORGANISM: Homo sapiens
US-09-833-381-1820
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US-08-213-419B-3/c
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                                                                                                                                                                                                                  1029 GAGTATCTGCTTCCCGGAACTTCTTGGACACCCTATAACTGAGTGCCCTGTTTCTTCATAAA
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                                                                                                                              Gaps
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Pred. No. 0.022;
0; Mismatches 60; Indels
                                                                              Query Match 2.8%; Score 42.2; DB 4; Length 1
Best Local Similarity 54.1%; Pred. No. 0.086;
Matches 86; Conservative 0; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08330108
; Sequence 1, Application US/08330108
; Patent No. 5795752
; GENERAL INFORMATION:
; TITLE OF INVENTION: IL-2-Stimulated Gene; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-08-956-171E-54
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,108
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,736
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EDNESS: single stranded
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Best Local Similarity 56.5%;
Matches 78; Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1562 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE
ORGANISM: hur
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US-08-330-108-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-330-108-1
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APPLICANT: Charles Kunsch

Gil H. Choi

Batrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
                                                                              ö
                                                                                                                                                               1296 IGAGIGACICAIGIAAIACICAITITITITITITITITITAACAICIIAITAATAGIAIGCIICIA 1355
                                                                                                                                                                                                                                                     2144 TTTTTTTTTTTTTTTTTTTTTAAGAGAATAAATCTAGAATATGACCTCTTTTTATTT 2085
                                                                                                                       1236 AAGTCAAAAAACAAGGGGTCTTGATTTATTTGGCGAACTTAAAGTTGCATTTATGTGTGA
                                                                                                                                                                                                                                                                                                                                           Score 45.4; DB 4; Length 6124;
Pred. No. 0.005;
0; Mismatches 136; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HV Vectra 486/33
OPBEATING SYSTEM:
MSDGS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME ASSETT OF COUNTRY 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2084 AATTATTCAAAAAAAATATATT 2062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-08-956-171E-54
Sequence 54, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
                             3.0%;
ilarity 48.3%;
Conservative
                             Query Match
Best Local Similarity
Matches 127; Conserva
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

Run on:

July 9, 2004, 21:00:33 ; Search time 519 Seconds (without alignments) 14067.586 Million cell updates/sec

US-09-914-098-55 1498 Title: Perfect score:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

3183909 seqs, 2436941669 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/USO7\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/DSO6\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/USO6\_NEW\_PUB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/USO6\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/DSO8\_NEW\_PUB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/USO8\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/USO9G\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/USO9G\_PUBCOMB.seq:\*

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12: /cgn2\_6/ptodata/1/pubpna/USO9G\_NEW\_PUB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/USO9\_NEW\_PUB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/USO9\_NEW\_PUB.seq:\*

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16: /cgn2\_6/ptodata/1/pubpna/USO9\_NEW\_PUB.seq:\*

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18: /cgn2\_6/ptodata/1/pubpna/USO9\_NEW\_PUB.seq:\*

19: /cgn2\_6/ptodata/1/pubpna/USO9\_NEW\_PUB.seq:\*

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10: /cgn2\_6/ptodata/1/pubpna/USO0\_NEW\_PUB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/USO0\_NEW\_PUB.seq:\*

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10: /cgn2\_6/ptodata/1/pubpna/USO0\_NEW\_PUB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/USO0\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 135471, Sequence 10439, A Sequence 135449, Sequence 6209, Ap Sequence 67243, A Sequence 11471, A Sequence 23, Appli Sequence 27991, A Sequence 2674, A Sequence 2674, A Sequence 26840, A Sequence 26840, A Sequence 26840, A Sequence 26840, A Sequence 26840, A Sequence 26840, A Sequence 26840, A Sequence 26840, A	
ΠD	US-10-424-599-135471 US-10-425-114-10439 US-10-425-114-6209 US-10-425-114-6209 US-10-425-114-6209 US-10-425-114-11471 US-10-425-114-28840 US-10-425-114-28840 US-10-425-114-28840 US-10-425-114-28840 US-10-425-114-26574 US-10-425-114-2048 US-10-425-114-2048 US-10-425-114-2048 US-10-425-114-2048	
1		
% Query Match Length DB	1593 1302 1303 14583 1515 1650 1650 1650 1650	
% Query Match	87777848888888888888888888888888888888	
Score	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
Result No.	0 1111111 11100400001004	

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TCGAAAAGTTTGTACAGAAAGATCAACCGGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTT 296

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177 GCCTCCGGCCTCCTTGTTAATCTCATTCAGGCAATATGCTATGTCGTCGTAAGGCCGGTG

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	-02	10-021-323-61	10-425-114-3566	-10-424-599-510	10-424-599-1236	-10-424-599-8706	09-294-093B-28	10-424-599-708	-986-076	1-667-494-1	7-462	1-667-464-1	798-029-1	-037-270-8	-117-722-84	-798-029-	-296-606-2	9-946-374-29	.0-015-395A-2	.0-206-915-33	.0-199-670-3	.0-201-858-33	.0-205-890-33	10-208-024-33	10-201-853-33	10-174-581-33	10-176-483-33	10-176-749-33	176-914-33	10-176-915-3	US-10-006-485A-296
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### ALIGNMENTS

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RESULT 1
US-10-424-599-135471
US-10-424-599-135471

Sequence 135471, Application US/10424599

Sequence 135471, Application US/10424599

Sequence 135471, Application US  

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 135471

LENGTH: 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 GGGCTGGGCATGGCTATTGCAGCGGCCGTGGTACCATTGGGCCTGCTTCTTC 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.9%; Score 1347.2; DB 13; Length 1593; Best Local Similarity 99.4%; Pred. No. 0; Mismatches B; Indels 0; (
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GITITACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCCTG 480
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                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: 700909008_FLI
US-10-425-114-10439
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Glycine max
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TCGAAAAGTTTGTACAGAAGGATCAACCGGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTT 404
                        TGGCTTGTTGGATGGGTTTCAGCTCAGCGTTCAGGTTGTCTTGGCAGCACTCTAGCTGTG
                                                                                           GTTCCTGCCATTTATGATGTAACAGTAGCCATCCCTAAGAGTTCCCCTGCTACAATG
                                                                                                                   ATGAAGAAATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTCAATGTGGTTTTCTGAGTAT
                                                                                                                                                                                                                     CAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCCTGTTCCTAGA
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                                                 TITCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAGAAGTGATATTGAT
                                                                                                                                    ATGAAGAAATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTCAATGTGGGTTTTTCTGAGTAT
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US-10-424-599-135449

i Sequence 135449, Application US/10424599

i Sequence 135449, Application US/10424599

i Sequence 135449, Application US/10424599

j Publication No. US20040031072A1

general Information:
    APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yinua

APPLICANT: Cao Yongwei

ITTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

ITTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 135449

LENGTH: 1394

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

CTHER INFORMATION: Clone ID: PAT_MRT3847_9331C.1

US-10-424-599-135449
TTCCTAGAAATGTTTTGATTCCAAGAACTAAGGGTTTTTGTTTCTGCAGTAAGTCATATGC
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Pred. No. 4.9e-281;
0; Mismatches 1; Indels 176; Gaps
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Matches 1295; Conservative
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RESULT 6
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; Sequence 11471, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Youguen E
; APPLICANT: Cao, Xongwen E
; APPLICANT: Cao, Xongwen E
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: UNMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 11471
; LENGTH: 1583
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COGANISM: Glycine max
FEATURE:
CTHER INFORMATION: Clone ID: 701127504_FLI
US-10-425-114-11471
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US-10-424-599-67243

i Sequence 67243, Application US/10424599

i Publication No. US20040031072A1

i GENERAL INFORMATION:

i APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

i TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 67243

LENGTH: 1750

TYPE: DNA

ORGANICM: Glycine max

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APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 9374
LENGTH: 1436
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
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CORGANISM: Glycine max
FEATURE:
COTHER INFORMATION: Clone ID:
US-10-425-114-9374
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Best Local Similarity 86.4%;
Matches 950; Conservative
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Sequence 3, Application US/08818581B

Publication No. US20020007499A1

GENERAL INFORMATION:

APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: BROWN, Adrian Paul
APPLICANT: BROWN, Adrian Paul
APPLICANT: KROON, Johannes Theodorus Maria
ITTLE OF INVENTION: 2-ACYLTRANSFERASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham Lidp
STREET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: US
ZIP: 10036
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-COMPAGINES
CORPETING SYSTEM: PC-COMPAGINES
CORPUTER: IBM PC compatible
OPERAING SYSTEM: PC-COMPAGINES
CORPETING SYSTEM: PC-COMPAGINES
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPC
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FILING DATE: M9-FB-1996
FILING DATE: 09-FEB-1995
FILING DATE: 09-FEB-1995
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Pred. No. 3.2e-158;
0; Mismatches 298;
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Similarity 73.4%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: 182..1316
US-08-818-581B-3
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Matches 821;
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Sequence 27991, Application US/10437963

Sequence 2791, Application US/10437963

Sequence 2791, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brabazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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FILLE REFERENCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963

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US-10-425-114-28840
; Sequence 28840, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Liu, Jingdong
; APPLICANT: Screen, Steven E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NOS: 73128
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; CTHER INFORMATION: Clone ID: LIB4765-008-H3_FLI
US-10-425-114-28840
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; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_32632C.1
US-10-437-963-27991 748 1002 1108 582 702 762 822 942 162 222 1408 1348 342 1288 402 1228 462 1168 1048 642 988 808 282 522 92 PP 8 6 8 6 8 6 8 \$ B \$ g & QΩ Б  $\overset{\sim}{\circ}$ qq  $\dot{\delta}$ g 8 QQ δ ò ò

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30.3%; Score 453.6; DB 13;
larity 70.1%; Pred. No. 1.4e-108;
Conservative 0; Mismatches 269;
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; Sequence 16071, Application US/10425114
; Publication No. US2004003488881
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Screen E
; APPLICANT: Screen E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Value
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 2048
; SEQ ID NO 2048
; LENGTH: 1220
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; OTHER INFORMATION: Clone ID: 700201362_FLI
US-10-425-114-2048
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US-10-425-114-2048
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ORGANISM: Zea
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                                             312 IGGIGGCAGGAGTIAAGGICCAAAIAITCACAGAICATGAAACCITITCGITIAAIGGGI
                                                                                          TGGTGGGCAGGCGTTAAGGTACAACTACATGCGGATGAGGAAACTTACCGATCAATGGGT
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 16071
LENGTH: 1646
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.7e-104;
es 269; Indels 4;
                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3061-054-H6_FLI
                                                                                                                                                                                                                                 Query Match 29.2%; Score 437.6; Best Local Similarity 69.5%; Pred. No. 2.7e Matches 623; Conservative 0; Mismatches
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Sequence 135460, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 135460
LENGTH: 717
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TAGITATATCTTGGGCGTGTCTGGTTGTGCGGGGTCTGTAAAGTTCCTGCAATGGTCTT 1107
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Pred. No. 3.4e-98;
0; Mismatches 44; Indels 98;
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// OTHER INFORMATION: Clone ID: PAT_MRT3847_9332C.1
US-10-424-599-135460
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Best Local Similarity 80.0%;
Matches 568; Conservative C
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US-10-021-323-14948

US-10-021-323-14948

Sequence 14948, Application US/10021323

Publication No. US20040123340A1

GENERAL INFORMATION:

APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.

APPLICANT: Fincher, Karen L.

APPLICANT: Fincher, Karen L.

APPLICANT: Pincher, Karen L.

APPLICANT: Pincher, Raren L.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With:

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION NUMBER: US/10/021,323

CURRENT APPLICATION NUMBER: US 60/255, 619

PRIOR RILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 14948

LENGTH: 581
                                                                                                         CITTCAACATCTTATCATAGTATGCTTCTATTCTATATATGTACTATTATGAATGCTTAT 1385
                                                                                                                                                                                                                                     CGATICATIGITITAATITAATIAGGATAICCITITGIATIGACAGICTAGGGGATGGC 1445
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.0%; Score 388.8; DB 17; Length 581; Best Local Similarity 80.5%; Pred. No. 1e-91; Matches 467; Conservative 0; Mismatches 112; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: LIB3829-018-Q6-K6-F2
US-10-021-323-14948
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ORGANISM: Gossypium hirsutum
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421 ATTACAGTGGCTATTCCCAAAAGCTCACCTTCACCTACAATGCTTAGACTTTTCAAGGGG 480
                                                                                                                                                            481 CAATCTTCTGTGGTACACGTACATATCAAACGACACCTCATGAAGGAACTGCCTGAAATG 540
                                                                                 CAACCTTCAGTGGTGCATGTTCATATCAAGAGGCATTTGATGAAGGAACTGCCAGATACA
                                                                                                                                                                                                                                                                                                 541 GATGAGGCTGTTGCACAATGGTGTAAAGATCTGTTTGTGG 580
                                                                                                                                                                                                                                          915 GAIGAGGCIGIIGCICAAIGGIGICGAGAIAIAITIGIGG 954
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July 9, 2004, 18:57:17 ; Search time 2827 Seconds
   (without alignments)
   15823.681 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	CA819096 sau68 BQ123121 EST60 B1974194 sai97 EG585493 EST48
Он	602 14 CA819096 739 13 BQ123121 570 12 BI974194 824 12 BG585493
e d	113 112 122
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Score	602 533.4 531.8
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99624 Zea may 95566 EST4873 40532 VRJ343T 85567 EST4873 23947 sal05e0 08939 si38bl1 00082 PCSC216	00176 Gm CK219 70126 CAB10003 03131 GA Ed00 10882 CAB20007 13846 EST33283 88651 GA ED00 20693 BNZO 053 36841 sav25c01 72320 RTCNT1 6 92810 sam64f01 86813 BN45 049	CE074283 EST00795 CF437515 EST673860 AW620973 S198e03.Y CA785831 Sat39h01. CD826229 BN25.063C CE654545 OSJNEC07C CE644085 OSJNEC07C CD820168 BN20.051G BF637273 NF047D10L BI405683 048D08 Ma CD831577 BN40.060B	53828 BJ463828 53828 BJ463828 140127 OSUNEDOS 54802 EBCa01 S 57887 ELOINO 52069 FGASO349 5858 SAK48D08 79456 V060D12 32848 OSUNEFIO
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#### ALIGNMENTS

RESULT 1

CA819096	
LOCUS	CA819096 602 bp mRNA linear EST 09-DEC-2002
DEFINITION	sau68h05.y1 Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID:
	Gm-c1071-6130 5' similar to TR:Q9SDN3 Q9SDN3
	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE. ;, mRNA sequence.
ACCESSION	СА819096
VERSION	CA819096.1 GI:26268033
KEYWORDS	BST.
SOURCE	Glycine max (soybean)
ORGANISM	Glycine max
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
	Glycine.
REFERENCE	1 (bases 1 to 602)
AUTHORS	Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
	Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
	Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
	Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
	Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
	McCann, R., Waterston, R. and Wilson, R.
TITLE	Public Soybean EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Shoemaker R/Public Soybean EST Project
	Public Soybean EST Project
	Washington University School of Medicine

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409 ATATIGATIGGCTIGTIGGAIGGGTTICAGCTCAGCGTTCAGGTTGTCTIGGCAGCACTC 468
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    739
    organism="Medicago truncatula"

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|cultivar="A17"
|db_xref="taxon:3880"
|clone="pgLSD-31M13"
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:3847"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1071-6130"
/tissue type="immature pods (~2cm long) of greenhouse grown plants"
/lab_host="H108"
/lab_host="Pector: pSPORT1; Site_1: NotI; Site_2: SalI; The cDNA library was constructed from mRNA isolated from immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life CDNA library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restrictions site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinios at Urbana-Champaign. email: l-vodkin@uiuc.edu"
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
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llarity 100.0%; Pred. No. 1.5e-93;
Conservative 0; Mismatches 0;
                                                                                                                                                                   Seg primer: -40RP from Gibco
High quality sequence stop: 445.
Location/Qualifiers
1. .602
                                                                                                                                                                                                                                                            organism="Glycine max"
                                                                                                                                                       www.resgen.com
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/clone lib="GLSD"
/olone lib="GLSD"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. cDNA was prepared from poly4+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Glgapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ123121 17-APR-2002 EST608697 GLSD Medicago truncatula cDNA clone pGLSD-31M13, mRNA
                                                                                                  Medicago truncatula
Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                          540
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TIGR sequence name: MTRAM79TK More information is available at:
www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
541 Trattriggcgaactraaagrigcarriargrigarigagrigacrcargraaracrcarra
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Grusak, M.A., Samac, D., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
ESTs from late stage developing seeds of Medicago truncatula Unpublished (2002)
Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713 798 7044
Fax: 713 798 7078
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/dev stage="25 to 35 days after pollination"
/lab_host="XLOLR"
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                                                                    TCTGAGTATCTTTTTCTGGAGAGAGATGGAGGCTGAAGGATGAAAGCACATTAAAGTCAGGC
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BI974194
sai97903.yl Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-9125 5' similar to TR:Q9XFW4 Q9XFW4
ACYL-COA:1-ACYLGLYCEROL-3-PHOSPHATE ACYLTRANSFERASE ;, mRNA BI974194.1 GI:16348599 sequence. BI974194 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Glycine max (soybean)
Glycine max
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,

Jobases 1 to 570)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoema, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., REFERENCE AUTHORS

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McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: estGwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 422. TITLE JOURNAL COMMENT FEATURES

64 Gaps , 0 Score 533.4; DB 12; Length 570; Pred. No. 8.7e-82; 0; Mismatches 1; Indels 0; 35.6%; Similarity 99.8%; 34; Conservative ( Query Match Best Local Simil Matches 534; C

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155 215 244 124 184 95 CCICCTTGTTAATCTCATTCAGGCAATATGCTATGTCGTCGTCAAAGGCCCGGTGTCGAAAAG CATGGCTATTGCAGCAGCAGCGTGGTACCATTGGCCCTGCTCTTCGCCTCCGG CATGGCTATTGCAGCAGCAGCGGCCGTGGTACCATTGGGCCTGCTTCTTCTTCGCCTCCGG GAGGTTCCGTTTGCTGACCTCGGAAATCCAAAGAGGGAAACTCACGTGTTTCGT Gredriccerrinecreaccreaccresaarccaaagesaaacreacegrerreer TGCGTTGTGCTCTGCTCCTTTTGGGCCTGGGCTTGGGCTTGG 125 156 185 36 65 g δ

| TGGATGGGTTTCAGCTTCAGGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAA 425

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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org, ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org, or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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262 AGACCGCTGTCAAAGAATTTGTACAGAAGGATCAACCGGGTGGTGGCAGAACTGTTGTGG 321
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Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
                                                                                                                                    CATGAAACCTTTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAGAAGT
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post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
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XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                     Medicago truncatula/Glomus versiforme mixed EST library Medicago truncatula/Glomus versiforme mixed EST library Eukaryota; mixed EST librarys.

Eukaryota; mixed EST libraries.

(bases 1 to 824)

Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.

ESTs from roots of Medicago truncatula after colonization with Glomus versiforme, 2001
                                                                                                                                                                                                   BG585493 824 bp mRNA linear EST 11-APR-2001 EST487257 MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone pMHAM-3019 5' end, mRNA sequence.

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/organism="Medicago truncatula/Glomus versiforme mixed EST
library"

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Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N380967e TIGR sequence name: MTDCE53TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                              ATCTTCAAAGTTTCTGCCGGTCATTGGCTGGTCAATGTGGTTTTCTGAGTATCTT
                                                                                         516 Arcticaagrircigccggrcarrggcrggrcaargrggrirrcrgagrarcrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
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                                       /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                ATGGATATTGGCCCAGCGCTCAGGGTGCCTTGGAAGTACACTCGCTGTCATGAAGAAGTC
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Library"
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larity 65.7%; Pred. No. 3.6e-80;
Conservative 0; Mismatches 373; Indels 3;
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Matches 720; Conserv
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/wol_type="mRNA"
/cultivar="Medicago truncatula genotype A17"
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/clone="pMHAM-3018"
/tissue_type="roots colonized with Glomus versiforme"
/tissue_type="roots colonized with Glomus versiforme"
/dev stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab host="E. coli strain XLOLR"
/lab host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xho1; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                           1110
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EST487330 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone pMHAM-3018 5' end, mRNA sequence.
BG585566
BG585566.1 GI:13600630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Utterback, T., Cho, J.
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ACTGGACAAGCATTTGGCAACAGGCACTTT---CGATGAGGAGATTAGACCTATTGGCCG
                                                                                                                    TCCAGTGAAATCATTGCTGGTGACCCTGTTCTGGTCGTGCTCCTGCTGTTTGGCGCCAT
                                                                                                                                                                                           AAAGTICCIGCAAIGGICTICGIIACICTICCIGGAAGGGTGIIGCATTITCAGCTIT
                                                                                                                                                                                                                                                                                                                                                                  ACCAATAAAGTCTCTTCTGGTAGTTATATCTTGGGCGTGTCTGGTTGTTGCGGGGTCTGT
                                                                                                                                                                                                                                              1148 IGGITIGGCAGTIGTTACTGCACTTATGCAAATICTGATTCAATTCTCAGAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago truncatula/Glomus versiforme mixed EST library
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.

1 (bases 1 to 780)
S Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T
and Fraser,C.M.

ESTS from roots of Medicago truncatula after colonization of
Glomus versiforme, 2001
Unpublished (2001)
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
The Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N381040e TIGR sequence name: MTDCF52TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

    780
/organism="Medicago truncatula/Glomus versiforme
library"

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1180
                                                                                                                                                                       /dev_stage="dormant"
/lab_host="DH10B"
/clone_lib="Vitis riparia endodormant bud - VRJ"
/clone_lib="Vitis riparia endodormant bud - VRJ"
/note="Organ: bud; Vector: pSport 1; Site_1: Sal1; Site_2:
Not1; VRJ is a cDNA library of Vitis riparia endodormant
buds. Endodormant buds were collected from insect and
disease free vines that were induced into dormancy with
short photoperiods. The directionally oriented library was
constructed according to Gibco BRL Superscript Plasmid
System for cDNA synthesis and plasmid cloning."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 485.8; DB 14; Length
Pred. No. 1.1e-73;
0; Mismatches 158; Indels
                                                   1. .739
/organism="Vitis riparia"
                                                                                              /mol_type="mRNA"
/db_xref="taxon:96939"
/clone="VRJ343"
                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1181 TCTGATTCAATTCTCACA 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.4%;
Best Local Similarity 78.6%;
Matches 580; Conservative
  Sed primer:
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Vitis riparia
Vitis riparia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 739)
Fennell, A. and Mathiason, K.
Expressed sequence tags from endodormant Vitis riparia buds
                                                                                                                                                                                                                                   250
                                                                                                                                                                                                                                                                                                                                                                                            347
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                                                                                                                                                                                  CTCTTCTTCGCCTCCGGCCTCCTTGTTAATCTCATTCAGGCAATATGCTCGTCGTA 227
                                                                                                                                                                                                                                                                                                                                      AGACCGCTGTCAAAGAATTTGTACAGGATCAACCGGGTGGTGGCAGAACTGTTGTGG 310
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Tel: 605 688 6373
Fax: 605 688 4713
Email: Anne_Fennell@sdstate.edu
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Horticulture, Forestry, Landscape and Parks Department
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Pred. No. 7.5e-75;
); Mismatches 84; Indels
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86.88;
Similarity 86.8
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683 706

623

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Glycine, Gloses 1 to 564)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

McCann, R., Waterston, R. and Wilson, R.

Unpublic Soybean EST Project
Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
South Memorial Parkway Huntsville, AL 35801 For further information call: (800) 533-4363 or contact: ccu@resgen.com web site:

www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 414.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM523947
sal05e03.yl Gm-c1057 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1057-4422 5' similar to TR:Q9SDN3 Q9SDN3
1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.;, mRNA sequence.
BM523947.1 GI:18727118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (soybean)
Glycine max
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                    TCTGAGTATCTTTTTCTGGAGAGAGTTGGGCCCAAGGATGAAAGCACATTAAAGTCAGGC 587
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CIGGAACITGITIGGCTIAITGAITGGIGGGCÜGGAGTIAAGGITGAAAIAIACACGGAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 TCTGAGTATCTTTTCCTGGAGAGAAGTTGGGCCAAGGATGAAAACACATTGAAATCAGGT
                                                                                     GATATTGATTGGCTTGTTGGATGGGTTTCAGCTCAGCGTTCAGGTTGTCTTGGCAGCACT
                                                                                                                                                                                                GATATTGATTGGCTTGTTGGGTTTTTAGCTCAGCGTTCGGGTTGCCTTGGCAGTACT
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                                                   CATGAAACCTTTCGTTTAATGGGTAAAGAGCATGCACTTGTGATAAGCAATCACAGAAGT
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/mol_type="mRNA"
/db_xref="taxon:3847"
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| TGTTCCCTAGAATGTCTTGA 763
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                                                                                                                                                                                                                                                                     Medicago truncatula/Glomus versiforme mixed EST library
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.

Eukaryota; mixed EST libraries.

Eukaryota; mixed EST libraries.

Eukaryota; mixed EST libraries.

Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.

ESTS from roots of Medicago truncatula after colonization with
Glomus versiforme, 2001

Unpublished (2001)
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Sol-221-7380
Email: mjharrisonanoble.org
Noble EST name: N381041e TIGR sequence name: MTDCF53TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

Location/Qualifiers

//organism="Medicago truncatula/Glomus versiforme mixed EST library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // mol_type="mRNA"
// wol_type="mRNA"
// cultivar="Medicago truncatula genotype A17"
// db_xref="taxon:119092"
// clone="pMHAM-30110"
// tissue_type="roots colonized with Glomus versiforme"
// dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
// lab_host="E. coli strain XLOLR"
// lb="Wector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                     EST487331 MHAM Medicago truncatula/Glomus versiforme mixed EST 11-APR-2001 library cDNA clone pMHAM-30110 5' end, mRNA sequence. BG585567.1 GI:13600631
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        CCTCATCAAATTCTCTCA 738
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역
                                                                                                                  /clone libe "Gm-c1057"

/note= "Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed From mRNA isolated
from degenerating cotyledons of 2 week old seedlings from
P1468916. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion.
The cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
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                               cotyledons, 2 week old
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 468; DB 12;
Pred. No. 1.4e-70;
0; Mismatches 60;
                                 'tissue_type="Degenerating
clone="SOYBEAN CLONE
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                                                              seedling" /
/lab host="DH10B"
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Best Local Similarity 89.4
Matches 504; Conservative
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AWS08939
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AW508939 620 bp mRNA linear EST 03-DEC-2001 si38bl1.yl Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-r1030-1174 5' similar to TR:Q40119 Q40119 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE ;, mRNA sequence.

GI:7147017

AW508939 AW508939.1 EST.

ACCESSION VERSION KEYWORDS

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1. .620
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-r1030-1174"
/lab_host="DH10B"
/clone="GENOME SYSTEMS CLONE ID: Gm-r1030-1174"
/lab_host="DH10B"
/clone="Wetcor: pSPORT1; Site_1: Sall; Site_2: Notl; This cDNA library was constructed from mRNA isolated from immature cotyledons of greenhouse grown plants (individual seed fresh weight of 100-300mg). The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. Sall linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-Sall restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note that Gm-r1030 is a re-rack of Gm-c1007."
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: estGwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 325.
                                                                                                             Johnson 1 (bases 1 to 620)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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4; Conservative
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AW695931.1
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                                                                                            Query Match
Best Local Simi
Matches 510;
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AW695931
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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COMMENT
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/cultivar="Hammond's Dwarf Scarlet"
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/dev_stage="6-days post-pollination"
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/note="Organ: Suspensor Region of Globular-Stage Embryos;
Vector: TriplEx2; Site_1: SfilA; Site_2: SfilB; Suspensor
regions were micro-dissected from globular-stage embryos
six days after pollination from greenhouse-grown plants
(Weterings et al., Plant Cell 13, 2409-2425 (2001)].
Double-stranded cDNA was synthesized from suspensor mRNA
using the SMART cDNA Library Construction Kit according to
the manufacturer (Clontech). The suspensor cDNA fragments
were directionally ligated into the Sfil restriction site
of the lambda TriplEx2 vector (Clontech), and the
recombinant cDNAs were transformed into E. coli XLI-Blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Estimations coccineus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Phaseolus.

I (bases I to 692)

SE Bui,A.Q., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S.,

MCElroy,K.E., Choi,P.S., Harada,J.J., Fischer,R.L. and

Goldberg,R.B.

Gene Activity in Different Regions of a Post-Fertilization Plant

Embryo by EST Analysis

Unpublished (2002)

Contact: Goldberg, R.B.

Department of Molecular, Cell, & Developmental Biology

University of California, Los Angeles

621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA

Tel: 310 825 3270

Fax: 310 825 3270

Fax: 310 825 3270
                                                                                                                                                                                                                                                                                                                                                                                                        CA900082
PCSC21606 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus coccineus cDNA 5' similar to Acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, mRNA sequence.
CA900082
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324
TATGGATGGCTCTCTGTGTAGAAGGAACTCGCTGTACACAGGGCCAACTATTAGCTGCTC
                                                                                                               crcaecerrcaecrreccrrescaecacrcrrecrereargaagaarcarceaegrrre
                                                                                              TOCCGGTCATTGGCTGGTCAATGTGGTTTTCTGAGTATCTTTTTCTGGAGAAGTTGGG
                                                                                                                                                             CCAAGGATGAAAGCACATTAAAGTCAGGCATCCAGCGACTGAGTGATTTCCCTCTTCCCT
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                                CTCAGCGTTCAGGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTC
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Seg primer: 5' TriplEx
POLYA=No.
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AW695931

NF100G06ST1P1051 Developing stem Medicago truncatula cDNA clone
NF100G06ST 5', mRNA sequence.
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
cells (Clontech). Suspensor cDNA plasmids used for directional sequencing were obtained by in vivo excision from the lambda TriplEx2 recombinants in E. coli BM25.8 cells (Clontech)."
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Contact: Dixon RA
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
Dixon,R.A.
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                                                                                                                                                Score 463.2; DB 14; Length
Pred. No. 8.8e-70;
Mismatches 78; Indels
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llarity 86.7%;
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H
                                                                                                                                                             /mol_type="mkNA"
/db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="NF100G06ST"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/clone_lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture internodal stem segments"
                                                                                                                                                                                                                                                                                                    Length 656;
                                                                                                                                                                                                                                                                                                   Score 461.2; DB 10; Length
Pred. No. 2e-69;
0; Mismatches 98; Indels
          The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 656 Std Error: 0.00
Plate: 100 row: G column: 06
Seg primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                /organism="Medicago truncatula"
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Biology Division
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Best Local Similarity 84.3%;
Matches 531; Conservative
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RESULT 13 CD400176/c

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/dev stage="two-week seedlings"
/lab_host="xil-Blue MRF' strain"
/lab_host="xil-Blue MRF' strain"
/clone lib="Soybean induced by Salicylic Acid"
/clone lib="Soybean induced by Salicylic Acid"
/note="Vector: pBluescript SK+; Site_1: EcoR I; Site_2:
Xho I; The cDNA library was constructed by He, C-Y from
mRNA isolated from two-week seedlings (cultivar Kefeng 1)
treated by spraying 2.0mM salicylic acid for 24, 36, 48
and 72 h. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI striction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into XLI-Blue MRF'
host cells (Stratagene)."
bp mRNA linear EST 07-JUN-2003 Salicylic Acid Glycine max cDNA 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1079
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                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                  Tian, A.-G., Wang, J., Cui, P., Han, Y.-J., Xu, H., Cong, L.-J., Huang, X.-G., Wang, X.-L., Jiao, Y.-Z., Wang, B.-J., Wang, Y.-J., Zhang, J.-S., Chen, S.-Y. and Yu, J. Soybean Expressed Sequence Tags Sequencing Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        China
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chen S-Y
Plant Biotechnology Laboratory
Institute of Genetics and Developmental Biology, CAS, (
Datun road, Beijing 100101, China
Tel: 86-10-64886859
Fax: 86-10-64873428
Email: sychen@genetics.ac.cn
Email: sychen@genetics.ac.cn
Seq primer: T7 primer.
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99.3%; Pred. No. 3.36
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466 b
Gm ck21948 Soybean induced by
mRNA sequence.
CD400176
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                                                                                                             CD400176.1 GI:31458148
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Glycine max
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Qy         122 GGGCATGGCTATTGCAGCGGCCGTGGTACCATTGGGCCTGCTCTTCTTCGCCTC         181           Db         48 GGATATGCAGTGCGGTTGCGTTGCGTTGCTTCTTCTTCTTCTTCTTCTT	Db   228   GCTTATTGGTGGGGGTTAGGATCCAACTGTACAGGATCCAGAACGTTTCG   287	2 TCTGGAGAGAGAGCCAAGGATGAAAGCACATTAAAGTCAGGCATCCAGCGCCTGÄG 60	67 685 3000 3000 31ca 1cc,	JOURNAL Unpublished (2000)  COMMENT Contact: Wing RA Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total High Quality bases = 521 Seq primer: TAATACGACTCACTATAGGG
Db 218 TTTATTTGGCGAACTTAAAGTTGCATTTATGTGTGAGTGA	RESULT 14 CB970126 LOCUS LOCUS LOCUS LOCUS CB970126 LOCUS CB970126 CB970126 CB970126 CB970126 ACCESSION CB970126 CB970126 CB970126.1 GI:30252575 KEYWORDS SOURCE ORGANISM Vitis vinifera ORGANISM Set andicotyledons; core eudicots;	rosids, Vitaceae; Vitis.  REFERENCE 1 (bases 1 to 670)  AUTHORS Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and Cook, D.  TITLE Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages  JOURNAL Unpublished (2003)  COMMENT Contact: Douglas Cook, PhD  CAES Genome Facility  UC Davis, Plant Pathology  One Shields Ave, Davis, CA 95616, USA  Tel: 530 754 6617  Fax: 530 754 6617  Email: drccok@ucdavis.edu  Seg primer: ACGGTACCGAATATGCC.	reation/Qualifiers  1670   Corganism="Vitis vinifera"     Mol type="mRNA"     Cullivar="Cabernet Sauvignon"     Cullivar="Cabernet Sauvignon"     Cullivar="Cabernet Sauvignon"     Colone="CAB10003 Ila=Fa_D05"     Sex="Hermaphrodite"     Abb_host="DH5alpha"     Clone lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"     Clone lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"     Clone lib="Cabernet Sauvignon Flower Site_1: Site_1: Site_2: Sfil; CAB1 is a cDNA library of Vitis     Vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples were collected approximately eleven days before onset of bloom (clusters at this stage were fully developed and flowers with calyptras or caps still attached. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:	5'-AAGCAGTGTATCAACGCAGTGGCCATTACGGCCGGG-3' and 5'-ATTCTAGAGGCCGAGGGCGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."  Query Match 29.1%; Score 436.4; DB 14; Length 670; Best Local Similarity 81.2%; Pred. No. 3.5e-65; Matches 506; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

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1. .685

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dpa"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 ITCTTCGCCTCCGGCCTCCTTGTTAATCTCAGGCAATATGCTATGTCGTAAGG 230
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High quality sequence start: 3
High quality sequence stop: 637.
Location/Qualifiers
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Search completed: July 9, 2004, 21:47:53 Job time : 2833 secs

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

July 7, 2004, 13:36:58; Search time 45 Seconds (without alignments) 2643.341 Million cell updates/sec US-09-914-098-56 1935 1 MAIAAAAVVVPLGLLFFASG......QSERSNPAKIVPAKSKNKGS 377 Run on:

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		Q9xfw4 brassica na	Q81g50 arabidopsis	Q40119 limnanthes	Q41745 zea mays (m	Q9sdn3 prunus dulc	Q9syc8 arabidopsis	Q9svx9 arabidopsis	Q39317 brassica na		Q9d517 m adult mal	Q7tt39 mus musculu	Q7zyil xenopus lae	Q9vv51 drosophila	Q7zwc9 brachydanio	Q9vv49 drosophila	Q8k4x7 m lysophosp
t-		Q9XFW4	Q8LG50	040119	Q41745	60Sed	Q9SYC8	6XAS6Ö	039317	Q7X9L2	Q9D517	Q7TT39	Q7ZYI1	Q9VV51	Q7ZWC9	Q9VV49	Q8K4X7
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* Query Match Length DR		390	389	377	374	306	376	310	311	237	376	376	376	386	377	380	378
% Query Match		81.0	80.8	78.5	75.0	0.69	0.99	60.0	59.8	43.6	31.3	31.0	30.8	30.7	30.3	29.9	28.5
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### ALIGNMENTS

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INARY; PRT; 390 AA.  Lrel. 12, Created) Lrel. 24, Last sequence upda Lrel. 3-phosphate acyltransf cerol-3-phosphate acyltransf pe).  lantae; Streptophyta; Embryc noliophyta; eudicotyledons; icales; Brassicaceae; Brassi siliques;  r A., Wolter F.P., Frentzen microsomal 1-acylglycerol-3 Brassica napus L."; 7) to the EMBL/GenBank/DDBJ 9138.1; -1-acylglycerol-3-phosphate C acyltransferase activity; IEA. metabolism; IEA. 3; Acyltransferase. Liransferase; 1. SC; 1. HIM basic. 2; HIM basic. 43771 MW; F1446E1B30009C3 43771 MW; F1446E1B30009C3 43771 MW; F1446E1B30009C3 vative 43; Pred. No. 2.9e-13	
INARY; PRT; 390 AA.  Lrel. 12, Created) Lrel. 24, Last sequence upda Lrel. 3-phosphate acyltransf cerol-3-phosphate acyltransf pe).  lantae; Streptophyta; Embryc noliophyta; eudicotyledons; icales; Brassicaceae; Brassi siliques;  r A., Wolter F.P., Frentzen microsomal 1-acylglycerol-3 Brassica napus L."; 7) to the EMBL/GenBank/DDBJ 9138.1; -1-acylglycerol-3-phosphate C acyltransferase activity; IEA. metabolism; IEA. 3; Acyltransferase. Liransferase; 1. SC; 1. HIM basic. 2; HIM basic. 43771 MW; F1446E1B30009C3 43771 MW; F1446E1B30009C3 43771 MW; F1446E1B30009C3 vative 43; Pred. No. 2.9e-13	
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MINARY; PRT;  Birel. 12, Create Birel. 12, Last a Birel. 24, Last a Birel. 3-phosphat  Ape).  Splantae; Streptop  Splantae; Streptop  Splantae; Streptop  Splantae; Brassica  a microsomal 1-ac  Fransica napus  11-acylglycerol-3  acyltransferase  incransferase acti  incransferase  11-acylglycerol-3  acyltransferase  incransferase  123; Acyltransfera  23; Acyltransfera  23; Acyltransfera  24; Hill basic.  15C; 1.  Hill 1; 1.  Transferase.  43771 MW; F14.	
MINARY;  BLrel. 12,  BLrel. 12,  BLrel. 24,  YCerol-3-ph  ape).  ape).  plantae; St  gloliophyta  sicales; Br  siliques;  siliques;  a microsoma  a microsoma  colliphyta  sicales; Br  apoliophyta  sicales; Br  apoliophyta  apoliophyta  sicales; Br  apoliophyta  apoliophyta  sicales; Br  apoliophyta  sicales; Br  apoliophyta  sicales; Br  apoliophyta  sicales; Br  apoliophyta  sicales; Br  Apoliophyta  sicales; Br  apoliophyta  sic	PRT;
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SULT 1  XFW4  O9XFW4;  O1-NOV-1999 (TrEMBLrel. 12, C 01-NOV-1999 (TrEMBLrel. 12, L 01-JUN-2003 (TrEMBLrel. 24, L 01-JUN-2003 (TrEMBLrel. 24, L 01-JUN-2003 (TrEMBLrel. 24, L 01-JUN-2003 (TrEMBLrel. 24, L 01-JUN-2003 (TrEMBLrel. 24, L EC 2,3.1.51).  EVAT.  EVAT.  EVAT.  EVAT.  Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Bra NCBL TaxID=3708;  [1]  SEQUENCE FROM N.A.  TISSUE=Developing siliques; Graefin zu Muenster A., Wolte "A cDNA encoding a microsomal acyltransferase of Brassica n Submitted (MAY-1997) to the E EMBL; 295637, CAB09138.1; - GO; GO:0003841; F:1-acylglyce GO; GO:0008415; F:acyltransferase GO; GO:0008415; F:acyltransferase GO; GO:0008415; F:acyltransferase GO; GO:0008152; P:metabolism; InterPro; IPR001092; HLH basi PROSITE; PS00038; HLH 1; 1. Acyltransferase; Transferase. SEQUENCE 390 AA; 43771 MM; Best Local Similarity 77.8%; Matches 288; Conservative 433	LT 1 W4 Q9XFW4 Q9XFW4;
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                                          WWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSS 122
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VIAAAVIVPLGLLFFISGLAVNLFQAVCYVLIRPLSKNTYRKINRVVAETLWLELVWIVD
                                                                               KFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLL
                                                                                                                                                                                                                           AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFK
                                                                                                                                                                                                                                                                                                                                                           GÓPSVVHVHIKCHSMKDLPESDDAIAÓWCRDOFVAKDALLDKHIAADTFPGOOEONIGRP
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-acyl-sn-glycerol-3-phosphate acyltransferase (Putative).
Limnanthes douglasii (Douglas's meadowfoam).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Limnanthaceae; Limnanthes.
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Arbunary 2015/19, Furned-75/19, Slabas A.R.;
"Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-phosphate acyltransferase from Limnathes douglasii.";
Plant Mol. Biol. 29:267-278(1995).
EMBL; Z48730; CAA88620.1; -.
EMBL; Z48730; CAA88620.1; -.
FIR; S60478; S60478.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001672; P:metabolism; IEA.
InterPro; IPR002123; Acyltransferase.
InterPro; IPR001092; HLH_basic.
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Pred. No. 5.3e-127;
3; Mismatches 41;
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SMART; SM00563; PlsC; 1.
PROSITE; PS00038; HLH 1; 1.
Acyltransferase; Transferase.
SEQUENCE 377 AA; 42780 MW; ODEC
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MEDLINE=96046746; PubMed=7579178;
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77.0%;
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       64
         AAAVWVPLGLLFFASGLLVNLIQAICYWWRPVSKSLYRRINRWAELLWLELWKLIDWW
                             AGVKVQI FTDHETFRLMGKEHALVI SNHRSDI DWLVGWVSAQRSGCLGSTLAVMKKSSKF
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1-acylcerol-3-phosphate acyltransferase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.
NCBI TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;

Feldmann K.;

Feldmann K.;

"Full-Length cDNA from Arabidopsis thaliana.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY084461; AAM61033.1; -.

R GO; GO:0008415; F:acyltransferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0018152; P:metabolism; IEA.

R GO; GO:0018152; P:metabolism; IEA.

InterPro; IPR001213; Acyltransferase.

R InterPro; IPR001092; HLH basic.

Pfam; PF01553; Acyltransferase; 1.

R MART; SM00563; PlsC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome annotation.";
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REA MEDLINE—95035993; bubbded=7948871;

RA

RISOlation and characterization of a maize cDNA that complements a 1-

RT acyl sn-glycerol-3-phosphate acyltransferase mutant of E.coli and

RT acyl sn-glycerol-3-phosphate acyltransferase mutant of E.coli and

RT acyl sn-glycerol-3-phosphate acyltransferases.";

RI Dant Mol. Biol. 26:211-223(1994).

REA EMBL, Z29518; CAA82638.1;

REA EMBL, Z29518; CAA82638.1;

REA GO:00008415; Ficayltransferase activity; IEA.

RO GO:00008415; Ficayltransferase activity; IEA.

RO GO:0016740; Fitransferase activity; IEA.

RO: GO:0016740; Fitransferase activity; IEA.

RO: GO:0016740; Fitransferase.

RO: GO:0008152; P:metabolism; IEA.

RO: GO:0008152; P:metabolism; IEA.

RO: GO:0008153; Acyltransferase.

RO: RomerPro: IPR001092; HLH basic.

REA RART; SM00563; PlsC; 1.

REA Acyltransferase; Transferase.

RW Acyltransferase; Transferase.

RW Acyltransferase; Transferase.

RW Acyltransferase; Transferase.

RW Acyltransferase; Transferase.

RW Acyltransferase; Transferase.

RW Acyltransferase; Transferase.

RW Acyltransferase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          FKGQPSVVHVHI KRHLMKELPDTDEAVAQWCRDI FVAKDALLDKHMAEGTFSDQELQDTG
                                                                                                                                                                                                                                                                                                                                                                                                 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE
                                                                                                            LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-acyl-glycerol-3-phosphate acyltransferase (Putative).
Zea mays (Maize).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tra
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 300
                                                                               300 RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVMHVFIMFSQAE 359
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                  81 MGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFL
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 241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG
                                                               RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE
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SEQUENCE FROM N.A.

Campalans A., Pages M., Messeguer R.;

"Identification of differentially expressed genes during dehydration almond (Prunus amygdalus) using the cDNA-AFLP technique.";

Submitted (DFC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF21337; AAF20003.1;

GO; GO:0008415; F:acyltransferase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001092; HIH basic.

InterPro; IPR001092; HIH basic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
11-acyl-sn-glycerol-3-phosphate acyltransferase.
Prunus dulcis (Almond) (Prunus amygdalus).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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306 AA; 33993 MW; CBD334496E25908D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.0%; Score 1336; DB 10; Best Local Similarity 84.5%; Pred. No. 8.5e-111; Matches 250; Conservative 23; Mismatches 23;
                                                                                                                                                                                                                                          PRT;
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                                                                                                                             RSNPAKIVPAKSKNK 375
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SEQUENCE 306 AA
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LLAAQEYAASQGLPAPRNVLIPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 WWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFLPVIGWSWWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 KFLPVIGWSMWFSEYLFLERNWAKDESTLKSGLQRLSDFPRPFWLALFVEGTRFTEAKLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFK 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 IKSLAVVLSWACVLTLGAIKFLHWAQLFSSWKGITISALGLGIITLCMQILIRSSQSERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 IAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERS
                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.

NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
11-acyl-sn-glycerol-3-phosphate acyltransferase.
Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 310;
                                                                                                                                                                                   SEQUENCE FROM N.A.
Benes V., Rechmann S., Borkova D., Ansorge W., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C., Quetier F., Salanoubat
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                N 14.)

N 14.)

A SEQUENCE FROM N.A.

A GU Arabidopsis sequencing project;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

NR EMBL; AL049660; CAB41190.1; -

DR PIR; T06755; T06755.

DR GO; GO:0008415; F:acyltransferase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR Hoterpro; IPR001092; HLH basic.

DR Interpro; IPR001092; HLH basic.

DR Pfam; PF01553; Acyltransferase; 1.

DR SMART; SM00563; PlsC; 1.

DR PROSITE; PS00038; HLH 1; 1.

Acyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1161.5; DB 10; Lengt; Pred. No. 3.1e-95; 30; Mismatches 35; Indels
1-acylcerol-3-phosphate acyltransferase-like protein.
F15B8.160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.3%;
Matches 228; Conservative 3
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283 TPAKVVPAKPKD 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDXHMAEGTFSDQELQDTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPIKSLLVVISWACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTALMOILIOFSOSE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LEAAQEYASIRSLPSPRNVLIPRTKGFVSAVSEIRSFVPAIYDCTLTVHNNQPTPTLLRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

A Stafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P., Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P., Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

Lunos S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

Example ACO06085; Ab330638.1; -.

BRBL; ACO06085; Ab330638.1; -.

BRBL; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; D96550; HLH basic.

BRART; SM00563; Plsc; 1.

BRART; SM00563; Plsc; 1.

BROSITE; PS00038; HLH 1; 1.

Acyltransferase; Transferase;

Acyltransferase; Transferase;

Acyltransferase; Transferase;
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                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 AA; 43435 MW; 0B9AE143B09ED4D0 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
               376 AA.
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                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress)
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les 228; Conservative
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Brown A.P., Brough C.l., Kroon J.T., Slabas A.R.;

Brown A.P., Brough C.l., Kroon J.T., Slabas A.R.;

Thosphate acyltransferase from rape.";

Submitted (JWN-1995) to the EMBL/GenBank/DDBJ databases.

EMBL; Z49860; CAA90019.1; -.

BMBL; Z49860; CAA90019.1; -.

RO; GO:0008415; F:acyltransferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase.

RO; GO:0016740; F:transferase.

RO; GO:0016740; F:transferase.

RO; GO:0016740; F:transferase.

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RO; GO:0016740; F:transferase.

RO; GO:0016740; F:transferase.

RO; GO:0016740; F:trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLIDWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 LPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QRSGCLGSALAVMKKSSKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 311;
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STRAIN=cv. PH 82-2-2; TISSUE=Seed;
Li J.R., Wang F., Li Q.Z., Zhang X.S.;
"Gene isolation and expression of 1-acy1-glycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31, Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-acyl-glycerol-3-phosphate acyltransferase (Fragment)
Triticum aestivum (Wheat).
              Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.8%; Score 1156.5; DB 1
61.4%; Pred. No. 8.8e-95;
ive 33; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 227; Conserv
eurosids II; Bra
NCBI_TaxID=3708;
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                                                                                                                       SEQUENCE
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Arakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Korno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Muramatsu M., Hayashizaki Y.,
A Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                   205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GFVSAVSIMRDFVPAIYDTTVIIPEDSFKPTMLRILQGQSSVVHVRIKRHSMSDMPNSDE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Adult male testis cDNA, RIKEN full-length enriched library,
clone:4930526L14 product:1-acylglycerol-3-phosphate O-acyltransferase
3, full insert sequence (1-acylglycerol-3-phosphate-gamma)
(EC 2.3.1.51) (1-acylglycerol-3-phosphate O-acyltransferase 3).
AGPAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDEKTLKSGLQRLKDFPRSFWLALFVEGTRFTPAKLLAAQEYAISQGLTAPRNVLIPRTK
                                                                                                                                                                                                                                                                                                                            86 ALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFLERSWA
                                                                                                                                                                                                                                                                                                                                                              KDESTLKSGIQRLSDPPLPFWLALFVEGTRFTQAKLLAAQEYATSTGLPVPRNVLIPRTK
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                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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H
                                                                                                                                                                                                          237;
                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                     35; Indels
acyltransferase.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF479037; AAP80656.1; -.
Acyltransferase; Transferase.
                                                                                                                                                 237 AA; 26693 MW; F4A164BDA47243A1 CRC64;
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                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                          Score 844.5; DB 1
Pred. No. 4.1e-67;
0; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 AA
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STRAIN=C57BL/6J; TISSUE=Head, Liver, and
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                             43.6%; Scc.larity 74.3%; Pre
Conservative 20;
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                                                                                                                                                                                                                                               Best Local Sim
Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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SEQUENCE
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Best Local S
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Q7TT39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 MWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAAQBYATST 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 GLPVPRNVLIPRIKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPIMLRLFKGQPSVVHVH 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
Lu B., Jiang Y.J., Chan M., Choy P.C.;
Lu B., Jiang Y.J., Chan M., Choy P.C.;
"Identification and characterization of 1-acylglycerol-3-phosphate acyltransferase-gamma.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK015906; BAB30025.2; -.
EMBL; AK075715; BAC35905.1; -.
EMBL; AK075715; BAC36329.1; -.
EMBL; AK076414; BAC36329.1; -.
MGD; MGI:1336186; Agpat3.
GO; GO:0003841; F:1-acylglycerol-3-phosphate O-acyltransferas. ..; IEA.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Yamamoto H., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa W., Chara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 IGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLIDWWAGVKVQI
annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.3%; Score 606; DB 11; Length 3 37.0%; Pred. No. 1.4e-45; ive 72; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002123; Acyltransferase. Pfam; PF01553; Acyltransferase; 1. SMART; SM00563; PlsC; 1.
                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-99279253; PubMed-10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 37.0
Matches 125, Conservative
              Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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RP SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hong L.,

RA Hopkins R.E., Jordan H., Moore T., Wax S.I., Wang J., Hong L.,

RA Hopkins R.S., Loquellano R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.N., Gay L.J., Hulyk S.W.,

RI Richards S., Worley K.C., Hale S., Garcia A.N., Gay L.J., Hulyk S.W.,

RI Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Holting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                             252 IKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKSLLVVIS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIDQATVDHFGKEHVVVILNHNFEIDFLCGWTMCERFGVLGSSKVLAKRELLCVPLIGWT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFLPVIGWS 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 GLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFKGOPSVVHVH 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLIDWWAGVKVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 376;
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC052382; AAH52382.1; -.
Hypothetical protein.
SEQUENCE 376 AA; 43247 MW; 3A03A08104FA65D3 CRC64;
                                                                                                                                                                     314 WATILL-----SPLFSFVLGVFASGSPLILIFL 342
                                                                                                                          312 WACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTAL 349
                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                             376 AA.
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Eukaryota, Metazoa, Arthropoda, Héxapoda, Insecta, Pterygc
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                       SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS)
                               CG4729.
Drosophila melanogaster (Fruit fly).
01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2003 (TrEMBLrel. 24, CG4729 protein (RE10780p).
                                                                                    NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GL PVPRNVL I PRTKGFVSAVSHMRSFVPA I YDVTVA I PKSSPAPTMLRLFKGQPSVVHVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 IKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHWAEGTFSDQELQDTGRPIKSLLVVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAAQEYATST
                       252 IKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKSLLVVIS
                                   GLPPLKYHLLPRTKGFTTAVQCLRGTVAA1YDVTLNF-RGNKNPSLLG1LYGKKYEADMC
                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Gaps
                                                                                                                                                      0/211;
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to 1-acylglycerol-3-phosphate O-acyltransferase 3.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                  30.8%; Score 595.5; DB 13; Length 34.4%; Pred. No. 1.2e-44; iive 79; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                     Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC043776; AAH43776.1; -.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILI 354
                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Acyltransferase.
SEQUENCE 376 AA; 43685 MW; 62ADFDCEBBBB460D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 WATILL-----SPLFSFVLGVFASGSPLILTFL 342
                                                               WACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTAL 349
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                                                                                                                                       376 AA.
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Q9VV51; Q9VV50;
01-MAY-2000 (TrEMBLrel. 13,
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                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
NCBL TaxID=8355;
                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                   SEQUENCE FROM PTISSUE=Embryo;
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Q7ZYI1
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STROUGHUE FROM N.A. (LUNG AND SHORT ISOURNES).

SEQUENCE STROWN N.A. (LUNG AND SHORT ISOURNES).

Adams Williams S.E., Holt R.A., Evans C.A., Gacayne J.D., Adams W.D. (Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Amanatides P.G., Scherer S.E., II P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Helt G. Ashburner M., Handerson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Barndon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Fleiffer B.D.,

RA Barndon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Fleiffer B.D.,

RA Ballew R.M., Basu A., Baxendal J., Barraktarancol C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., Baxendal J., Barraktarancol C.R., Miklos G.L.G.,

RA Beeson K.Y., Bernos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Ra Ballew R.W., Busan D.A., Bernen B.P., Bhandari D., Bolshakov S.,

Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Glodek A., Gong F., Gorrell J.H., Gadicu E., Center A., Dan R.

Rolsen K.J., Barvey D., Heiman T.J., Wei M.-H., Ibedwan C.,

Hostin D., Harvey D., Heiman T.J., Wei M.-H., Ibedwan C.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Ra Glodek A., Gong F., Gorrell J.H., Olz C., Gannison J.A., Ketchum K.A.

Ra Mattei B.L., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko D., Lei Y. Levitsky A.A., Li J., Li Z., Liang Y.,

Ra Mattei B.W., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

Ra Mattei B.C., Siden Kianos M., Strong R., Suns K.,

Ra Alazzolo M., Pittman G.S., Pan S., Rollad Y., Worlest W.,

Ra Rairer M., Rollad A.C., Stapleton M., Strong R., Suni B.,

Ra Shier E., Spradling A.C., Stapleton M., Strong R., Suni B.,

Ra Shier E., Spradling A.C., Stapleton M., Strong R., Zho S., Zhan M., Wang Z.,

Ra Globe R., Myore E., Stapleton M., Strong R., Zhao S., Zhao S., Zhao M.,

Rang C., Wang S., Wang S., Rulb S., Zhao S., Zhao S., Zhao S., Zhao S., Zhao S., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=y,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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EMBL; AE003527; AAF49472.1; -.
EMBL; BT001546; AAN71301.1; -.
FlyBase; FBgn0036623; CG4729.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Last sequence update) Last annotation update)

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LGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLIDWWAGVKVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09VV49;
01-MAY-2000 (TrEMBLrel. 13, C;
01-MAY-2000 (TrEMBLrel. 13, L;
01-JUN-2003 (TrEMBLrel. 24, L;
CG4753 protein (RE72803p).
CG4753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 KIVPAKSKN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GNVEAKKEN 377
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                                                                               72
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12
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                                                                                                                                                                                                                                                                                                                                                                                                                       SMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAAQEYATS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQI-LIQFSQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : ||: : | | : : | | :: | | :: | 313 KRRLCSLVNFVCWAVFSLSCIFYYVITSLLAANW------TAFITALSVLGLFYWLM 363
                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                         12 LGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLIDWWAGVKVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLPVPRNVLIPRIKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAP-TMLRLFKGQPSVVH
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                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to 1-acylglycerol-3-phosphate O-acyltransferase 3.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                            28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 377;
                                                                                                                                                                   Length 386;
                                                                                                                                                               30.7%; Score 595; DB 5; Length 386
32.5%; Pred. No. 1.4e-44;
tive 95; Mismatches 133; Indels
                                                                                 Missing (in isoform Short). /FTId=VSP 050280. 1E94370E971C35D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43849 MW; 1B3B96615A60CA6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.3%; Score 587; DB 13; I 33.9%; Pred. No. 6.9e-44; ive 82; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2003) to the EMBL/GenBank/DDBJ da EMBL; BC049474; AAH49474.1; -. GO; GO:0008415; F:acyltransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0008152; P:metabolism; IEA. InterPro; IPR002123; Acyltransferase. InterPro; IPR02123; Acyltransferase. Pfam; PF01553; Acyltransferase; I. SMART; SM00563; PlSC; I.
                 Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; P1sC; 1.
Hypothetical protein; Alternative splicing.
VARSPLIC 1 243 Missing (in is
IPR002123; Acyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : |: |: |: |: |: |: |: 364 GQAINKTQI--SKASNYGS 380
                                                                                                                         386 AA; 44397 MW;
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Best Local Similarity 32.55
Matches 123, Conservative
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Matches 125; Conservative
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enhmitted (MAR-2003)
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InterPro;
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RX Anderskeley 1.

RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Pandell M.D., Zhang Q., Chen L.X.,

RA Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Apbayani A., Helf, M.D., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Apbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.W., Basu A., Barman B.P., Bhandari D., Bolshakov S.,

RA Borson K.Y., Benos P.V., Berman B.P., Cadleu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Butler H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Bongelista C.C., Ferriara C., Ferriara S., Fleischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Marphy B., Murphy L., Morsherson D.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Morsher, Paland M.,

RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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71
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                                                                                                                                                                                                                                                                                                                FIDHETFRIMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFLPVIGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 MWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAAQEYATST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLPVPRNVL1PRTKGFVSAVSHMRSFVPA1YDVTVA1PKSSPAPTMLRLFKGQPSVVHVH
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Last sequence update)
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Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Mulliams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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A we J., Yeh R.-F., Zaveri J.S., Zhun M., Zhou X., Zhu S., Zhu X., Smith H.O.,
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A Miranda A., Mungall C.J., Nunco J., Pacled J., Paragas V., Park S.,
R. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
B. Flybase, Faphrolaces, Phousnehavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
R. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R. Shybase, Empholaces, P. C., Sarik J. S.,
R. Shybase, Faphrolaces, Acyltransferase activity; IEA.
BREN, Republes, Prouctabolism; IEA.
R. InterPro; Pro0212; Acyltransferase.
BREN, Remi, PPO153; Acyltransferase.
BREN, Remi, PPO153; Pacyltransferase.
BREN, Remi, PPO153; Pacyltransferase.
BREN, Remi, PPO153; Pacyltransferase.
BREN, Remi, PPO153; Pacyltransferase.
BREN, Remi, PPO153; Pacyltransferase.
BREN, Remi, PPO153; Pacyltransferase.
BREN, Remi, PRO153; Pacyltransferase.
BREN, Remi, PRO153; Pacyltransferase.
BREN, Remi, PRO153; Pacyltransferase.
BREN, Remi, PRO153; Pacyltransferase.
BREN, Remi, PRO153; Pacyltransferase.
BREN, Remi, PRO1
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132 VWWMAEFIFLDRNFEKDKVVIKTQLKEVFSYPDPVWLLLNAEGTRFTPAKHELSVKFAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.9%; Score 579; DB 5; Length 380; Best Local Similarity 32.5%; Pred. No. 3.6e-43; Matches 121; Conservative 84; Mismatches 151; Indels
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

July 7, 2004, 13:33:37 ; Search time 18 Seconds (without alignments) 1090.580 Million cell updates/sec Run on:

US-09-914-098-56 1935 1 MAIAAAAVVVPLGLLFFASG......QSERSNPAKIVPAKSKNKGS 377 Title: Perfect score: 1 Sequence: 1

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues

Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		nrz7 homo sapien	s homo	. rattu	Q9nuq2 homo sapien	mus m				esche		3333 saccharomyc								z7g4 chlamydia p	drosophil	drosophil	drosophil	drosophil	1716 drosophila					bacil		mus n	P22174 infectious	4958 saccharomyc
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P33453 uukuniemi v	Q22949 caenorhabdi	Q93841 caenorhabdi	P20471 rhizobium m	Q8fxx4 brucella su	P96289 mycobacteri	P51829 mus musculu	O53609 mycobacteri	Q7u2x8 mycobacteri	Q8ye74 brucella me	Q8cjg1 mus musculu	Q8d9g5 vibrio vuln
RRPL UUK	PLSB_CAEEL	PLC1_CAEEL	NDVB RHIME	SYFB_BRUSU	MML7 MYCTU	CYA7_MOUSE	Y064 MYCTU	X065_MYCBO	SYFB_BRUME	I2C1 MOUSE	PYRD_VIBVU
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06	89 0.	68	80	88.5	88.5	88.5	œ œ	88	87.5	87.5	87
34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Pransmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
-!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate
CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
-!- PATHWAY: De novo phospholipid biosynthesis; second step.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                            SINILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate acyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.5%; Score 628; DB 1; Length 376; Best Local Similarity 37.6%; Pred. No. 2.1e-47; Matches 127; Conservative 75; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform Gamma-2)
                                                                                                                                                                                                                                                                                                               Phospholipid biosynthesis; Transferase; Acyltransferase; Transmembrane; Alternative splicing.
TRANSMEM 15 39 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                   C12CDBB7CC363852 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 WACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTAL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 AA
                                                                          IsoId=Q9NRZ7-1; Sequence=Displayed;
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                                                                                                                                                                                                                          EMBL; AF156774; AAF80336.1; -.
EMBL; AF156775; AAF80337.1; -.
EMBL; AB040138; BAB18943.1; -.
EMBL; BC011971; AAH11971.1; -.
Genew; HGNC:326; AGPAT3.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                     376 AA; 43381 MW;
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Q9NRZ5;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                 Name=Gamma-2;
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altaschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Scheetz T.E.,

X Aspleton M., Soares M.B., Bonaldo M.F., Carning L., Scheetz T.E.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., MocBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Helton E., Young A.C., Shevchenko Y., Bouffard G.G.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Blakesley R.W., Touchman J.W., Schmutz J., Morra M.A.,

X Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

X Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Rodriguez A.C., Grimwood J., Schmutz J., Morra M.A.;

R Rodriguez A.C., Grimwood J., Schmutz J., Morra M.A.;

R Rodriguez A.C., Grimwood J., Schmutz J., Morra M.A.;

R Rodriguez A.C., Grimwood J., Schmutz J., Morra M.A.;

R Rodriguez A.C., Grimwood J., Schmutz J., Morra M.A.;

R R Human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic aidlaintivil
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase delta (EC 2.3.1.51) (1-AGP acyltransferase 4) (1-AGPAT 4) (Lysophosphatidic acid acyltransferase-delta) (LPAAT-delta) (1-acylglycerol-3-phosphate O-acyltransferase 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure and functions of lysophosphatidic acid acyltransferases."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

    similarity).
    -!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate
    COA + 1,2-diacyl-sn-glycerol 3-phosphate.
    -!- PATHWAY: De novo phospholipid biosynthesis; second step.
    -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
    -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate acyltransferase family.

                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phospholipid biosynthesis; Transferase; Acyltransferase;
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SMART; SM00563; PlsC; 1.
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                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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378 AA;
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28.7%; Score 554.5; DB 1; Length 378;

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                                                                                                     PRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGGSKVLAKKELAYVFIIGWMWYF
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                                    15 LFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLIDWWAGVKVQIFTD
                                                     75 HETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFLPVIGWSMWF
                                                                                                                                         SEYLFLERSWAKDESTLKSGIORLSDFPLPFWLALFVEGTRFTOAKLLAAOEYATSTGLP
            Gaps
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           94; Mismatches 148; Indels
  31.6%; Pred. No. 5.8e-41
             114; Conservative
Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li W., Suzuki T.;
"Rattus norvegicus mRNA for lysophosphatidic acid
acyltransferase-delta, complete cds.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic acid by incorporating acyl moiety at the 2 position (By
                                                                                                                                                                                                                                                                                                 2.3.1.51)
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CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate
CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
PATHWAY: De novo phospholipid biosynthesis; second step.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase delta (EC 2.3.1.51)
AGP acyltransferase 4) (1-AGPAT 4) (Lysophosphatidic acid
acyltransferase-delta) (LPAAT-delta) (1-acylglycerol-3-phosphate (
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Li W., Suzuki T.;
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   28.5%; Score 551.5; DB 1; 33.7%; Pred. No. 1.1e-40; iive 81; Mismatches 138;
                                                      Best Local Similarity 33.7
Matches 114; Conservative
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TRANSMEM TRANSMEM TRANSMEM TRANSMEM SEQUENCE

Transferase;

IPR002123; Acyltransferase.

Pfam; PF01553; Acyltransferase; 1. SMART; SM00563; PlsC; 1. Phospholipid biosynthesis; Transfe

Transmembrane

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09NUQ2; Q8IZ47; Q9BQ4;
28-FEB-2003 (Rel. 41, Traated)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon (EC 2.3.1.51)
(1-AGP acyltransferase 5) (1-AGPAT 5) (Lysophosphatidic acid
acyltransferase-epsilon) (LPAAT-epsilon) (1-acylglycerol-3-phosphate
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Catarrhini, Hominidae, Homo.
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MEDLINE=21154917; PubMed=11230166;
Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and expression of LPAAT-epsilon."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŗ.,
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                                                                            364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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Patent number WO9932644,
                                                                            STANDARD;
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SEQUENCE FROM N.A.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: It is uncertain whether Met-1 or Met-12 is the initiator.
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90A0F87FC7C78081 CRC64;
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EMBL; AL136587; CAB66522.1; -.
EMBL; AK002072; BAA92069.1; ALT_INIT.
EMBL; BC023550; AAH23550.1; -.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PISC; 1.
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61 81 PC
344 364 PC
156 156 L
364 AA; 42072 MW;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human TISSUE=Placenta;
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases. and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic acid by incorporating acyl moiety at the 2 position (By similarity).

-!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate = COA + 1,2-diacyl-sn-glycerol 3-phosphate.
-!- PATHWAY: De novo phospholipid biosynthesis; second step.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate Wambutt R., Korn B., Klein M., Poustka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001). TISSUE=Brain; MEDLINE=22388257; PubMed=12477932; SEQUENCE FROM N.A. SEQUENCE FROM N.A.

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A CAZZAKI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D. P., Bult C., Hume D.A., Quackenbush J.,

A Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Gasterland T., Cariboldi M., Gissi C., Godzik A., Gough J.,

A Kanai A., Kawaji H., Kawasawa N., Hirokawa N., Jackson I.J., Jarvis E.D.,

A Kanai A., Kawaji H., Kawasawa N., Henhard B., Lyons P.A.,

A Kanai A., Kawaji H., Marchionni L., McKenzie L., Miki H.,

A Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Betrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

A Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yangi I., Yangi L.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yangi I., Yangi L.,

Yuan Z. Zavolan M., Zhu Y., Zimmer A., Carninci P. Havatsu
                                                                                                     116
                                                                                                                                                                                                                           175 RFT--QAKLL-AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPALYDVTVAIP-- 229
                                                                                                                                                                                                                                                                                                                                                                                                                       236 DDGGQRRESPTMTBFLCKECPKIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIE- 294
                                                                                                                             62 VLFFFENYTGVQILLYGDLP----KNKENIIYLANHQSTVDWIVADILAIRQNALGHVRY
                                                                                               57 LVWLIDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLA
                                                                                                                                                                                            117 VMKKSSKFLPVIGWSMWFSEY--LFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGT
                                                                                                                                                                                                                                                                                                                                            176 RYNPEÓTKVLSASÓAFAAORGLAVLKHVLTPRIKATHVAFDCMKNYLDAÍYDVTVVYEGK
                                                                                                                                                                                                                                                                                                                                                                                         230 ----KSSPAPTMLRLFKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PECE MOUSE STANDARD; PRT; 365 AA.

PECE MOUSE STANDARD; PRT; 365 AA.

Q9DDIE8; Q8BG61; Q8CGN6;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon (EC 2.3.1.51)
(1-AGP acyltransferase 5) (1-AGPAT 5) (Lysophosphatidic acid
acyltransferase-epsilon) (LPAAT-epsilon) (1-acylglycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=NVMRI;
Lu B., Jiang Y.J., Chan M., Choy P.C.;
"Identification and characterization of 1-acylglycerolphosphate acyltransferase-epsilon.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                    18;
      Length 364;
  15.7%; Score 304; DB 1; Length 36.
28.8%; Pred. No. 4.5e-19;
ive 65; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 FYESPDPERRKRFPGKSVNSKLSI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 MAEGTFSDQELQDTGRPIKSLLVV 309
Query Match
Best Local Similarity 28.8<sup>3</sup>
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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RECEIVENCE FROM N.A.

SITRAIN=CZech II; TISSUE=Mammary gland;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Boxins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carnind G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Paltaron D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Plakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

Samilarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate = CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
-:- CAA + 1,2-diacyl-sn-glycerol 3-phosphate.
-:- PATHWAY: De novo phospholipid biosynthesis; second step.
-:- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-:- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate acyltransferase family.
-:- CAUTION: It is uncertain whether Met-1 or Met-12 is the initiator.
                                                                                                                                            Ö
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of the Hayashizaki Y.;" "Analysis of the Mouse transcriptome based on functional annotation of the Mouse transcriptome based on functional annotation of the Mouse transcriptome based on functional annotation of the Mature 420:563-573 (2002).
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POTENTIAL.
L -> W (IN REF. 1).
L -> M (IN REF. 1).
W, C13E14759610E19B CRC64;
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EMBL; AK003649; BAB22915.2; -...
EMBL; AK082137; BAC38421.1; -...
EMBL; AK08985; BAC40983.1; -...
EMBL; BC031987; AAH31987.1; ALT_INIT.
MGD; MGI:1196345; D8Ertd319e.
InterPro; IPR002123; Acyltransferase.
Ffam; PF01553; Acyltransferase; I...
SMARI; SM00563; P1SC; 1...
Phospholipid biosynthesis; Transferase;
Transmembrane.
TRANSMEM 345 365 POTENTIAL.
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CONFLICT
SEQUENCE
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Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomyces.

CSI\_TaxID=4932;

SEQUENCE FROM N.A. STRAIN=S288c

01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 45.5 kDa protein in FATI-TCM62 intergenic region.

STANDARD;

YEAST

YBP2 YE P382<u>2</u>6;

159 SDFPLPFWLALFVEGTRF - TOAKLL - AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMR

46 LYQRVDDRLYCVYQNMVLFFFENYTGVQILLYGDLP----KNKENVIYLANHQSTVDWIV

LYRRINRVVAELLMLELVWLIDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLV

102 ADMLAARQDALGHVRYVLKDKLKWLPLYGF--YFAQHGGIYVKRSAKFNDKEMRSKLQSY 101 GWVSAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEY--LFLERSWAKDESTLKSGLQRL

220 SHLDAIYDVIVVYBGNEKGSGKYSNPPSMTEFLCKQCPKLHIHFDRIDRNEVPEEQEHMK 279 SFVPAIYDVIVAIP-----KSSPAPIMLRLFKGQPSVVHVHIKRHLMKELPDTDEAVA 268

216

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8

40 40 40

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 VVVP-LGLLFFASGLLVNLIQAICYVVVRPVSKSLY-----RRINRVVAELLWLELV-W
                                                                                                                                                                              Andre B., Cziepluch C., Hein C., Jauniaux J.-C., Urrestarazu A., Vissers S., Vissers S., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate acyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z35911; CAA84984.1; -.
PIR; S45900; S45900.
GermOnline; 138585; -.
SGD; S0000246; YBR042C.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
Hypothetical protein; Phospholipid biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04CADDD1247D98A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 271; DB 1; L. 24.6%; Pred. No. 3.9e-16; Ative 72; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 AA; 45515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87; Conservative
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78
138
397
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Gaps

15.7%; Score 303; DB 1; Length 365; 30.7%; Pred. No. 5.6e-19; Live 57; Mismatches 101; Indels 18;

Conservative

Query Match Best Local Similarity Matches 78; Conserv

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POTENTIAL.
POTENTIAL.
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 47
89
143
992
45938 MW;
                                                                        12.8%;
25.8%;
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 27
69
123
372
396 AA;
                                                                                      Similarity
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                                                                                               85;
                                                                                                                                              33
                                                                                                                                                                                                                                                                                                                 222
            TRANSMEM
TRANSMEM
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                                                                                                                                              245
                                      LIDWWAGVKVQIFTDHE----TF----RLMG--KEHALVISNHRSDIDWLVGWVSA 105
                                                                                     -- FPLPFWLALFVEGTRFTQAKLLAAQEYATSTG 192
                                                                                                                                                                  193 LPVPRNVLIPRIKGFVSAVSHMRSFVPAIYDVTVAIP--KSSPAPIMLRLFKG-----Q 244
                                                                                                                                                                                         246 KKPFKNVLLPHSTGLRYSLOKLKPSIESLYDITIGYSGVKQEEYGELIYGLKSIFLEGKY 305
WWPGISLLIFFQGCLILLFLQLTY-----KTLYCRNDIRKQIGLNKTKRLFIVLVSS 65
                                                                                                                                       186 GSLAGKSPERITEEGESIWNPEVIDPKQIHWPYNLILFPEGTNLSADTRQKSAKYAAKIG
                                                                     106 QRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97051598; PubMed=8896275;
Eide L.G., Sander C., Prydz H.;
"Sequencing and analysis of a 35.4 kb region on the right arm of chromosome IV from Saccharomyces cerevisiae reveal 23 open reading
                                                                                                                                                                                                                                 PSVVHVHIKRHIMKELPDTDE-AVAQWCRDIFVAKDALLDKHWAEGTF-SDQE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 12:1085-1090(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
acyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z49770; CAA89843.1; -.
PIR; S54641; S54641.
Germonline; 140509; -.
SGD; S0002425; YDR018C.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SWART; SM00563; PlsC; 1.
Hypothetical protein; Phospholipid biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Hypothetical 45.9 kDa protein in KCS1-GCV1 intergenic region.
YDR018C OR YD9335.04C OR PZF396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dedman K., Brown D., Hamlyn N., Bowman S., Barrell B.G., Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                    396 AA
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Q12185;
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                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                  ETFRLMG------KEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKF
                                                                                                                                                                                                                                                                                                                                                                          17 FASGLLVNLIQAICYVVVRPVSKSLYRR-INRVVABLLWLELVWLIDWWAGVKVQIFTDH
                                                                                                                                                                                                                                                         FISGSLSIVVEQICLQVLLPWSKIRFQNGINQSKKAFIVL-LCMILNMVAPSSLNV--TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 FWLALFVEGTRF---TQAKLLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDVIVAIPKSSPAP------TMLRLF--KGQPSVVHVHIKRHLMKELP-DTDEAVAQ
                                                                                                                                                      Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Bone marrow;

MEDLINE=97191544; PubMed=9039502;

Magase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;

Prediction of the coding sequences of unidentified human genes.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced lanalysis of cDNA clones from cell line KG-I and brain.";
                                                                                                                                                        54;
                                                                                        Length 396;
                                                                                                                      ; Pred. No. 4.9e-14;
61; Mismatches 129; Indels
POTENTIAL.
9F55AB56C8FD44DD CRC64;
                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 LPVIGWSMWFSEYLFLERSWAKDESTL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y205_HUMAN
ID Y205_HUMAN STANDARD; PRT; 370 AA.
AC Q92604;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein KIAA0205.
GN KIAA0205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 WLIGVWKEKDQLLEDYYNTGQFKSNAKND 354
                                                                                           Score 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 WCRDIFVAKDALLDKHMAEGTFSDQELQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVIGWSMWFSEYLFLERSWA--------KDES--TLKSGIQ---RLSDFPL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VVAQMMWLMDHIFKYTNFGIVSLVHGDFFIRQGRSYRDQQLLLLKKHLENNYRSRDRK- 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A------IYDVTVAIPKSSP--APTMLRLFKGQPSVVHVHIKRHLMKELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLFFASGLLVNLI---QAICYVVV----RPVSKSLYRRINRVVAE-LLWLELVWLIDWWA
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
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EMBL; BC034621; AAH34621.1; -.
InterPro; IPR002123; Acyltransferase.
SMART; SM00563; PlsC; 1.
Hypothetical protein; Phospholipid biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.6%; Score 186.5; DB 1; Length 23.6%; Pred. No. 8.8e-09; tive 58; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93498544EA651541 CRC64;
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01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yihG.
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                                                                                                                                                                                                                                                                                                                                                                          acyltransferase family.
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Best Local Similarity
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ID YIHG ECOLI
AC P32129;
DT 01-OCT-1993
DT 16-OCT-2091
DE HYPOTHETICAL
GN YIHG OR B386
OS ESCHETIAN
OC BACTETIAN
OC ENTEROBACTEX
OX NCBI_TAXID=5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 LGSTLAVMKKSSKFLPVIGWSMWFSEYLFLER------SWAKDESTLKSGIQRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFPL-PFWLALFVEGTRFTQAKLLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 IPMNKYFLKQQLAWVPFLGLACWSLDMPPMKRYSRAYLLRHPERRGKDVETTRRSCEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 PAIYDVIVAIPKSSPAPTMLRLFKGQPSVVHVHI-------KRHLMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AAVVVPLGLLFFASGLLVNLIQAICYV--VVRPVSKSL-----YRRINRVVAELLWLEL
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Rhabditidae; Peloderinae; Caenorhabditis.
P SEQUENCE FROM N.A.

C STRAIN=K12 / MG1655;

RX MEDLINE=93347969; PubMed=8346018;

RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;

RT "Analysis of the Escherichia coli genome. III. DNA sequence of the RT region from 87.2 to 89.2 minutes.";

RT region from 87.2 to 89.2 minutes.";

RL Nucleic Acids Res. 21:3391-3398(1993).

CC -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate

CC --- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate

CC --- syltransferase family.

CC --- richtongh a coll acyltransferase family.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 44.7 kDa protein C01C10.3 in chromosome X.
C01C10.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 310 AA; 36289 MW; 9F8E3F52EB0B186E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%; Score 148; DB 1; L
21.6%; Pred. No. 1.6e-05;
iive 58; Mismatches 115;
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PIR; S40808; S40808.
ECOGene; EG11833; yihG.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L19201; AAB02997.1; -.
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
(1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 6.4%; Score 124.5; DB 1; Length 391; Local Similarity 21.4%; Pred. No. 0.0025; Loservative 57; Mismatches 160; Indels 73;
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                                                Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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WormPep; C01C10.3; CE02449.
InterPro; IPR002123; Acyltransferase.
SMART; SM00563; PlsC; 1.
Hypothetical protein.
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REMBL; Z74100; CAA98614.1; -.

REMC, Z74100; AA8600.

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Recrmonline; 140294; -.

Recrmonline; 14
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-!- FUNCTION: May be an acyltransferase with an altered substrate specificity that enables it to use a C-26-CoA in place of the C-16 or C-18-CoAs used by the wild type protein.

-!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate CoA + 1,2-diacyl-sn-glycerol 3-phosphate.

-!- PATHWAY: De novo phospholipid biosynthesis; second step.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate acyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 Q -> L (IN ALLELE SUPPRESSOR SLC1-1).
33887 MW; 36ECBBC2659655EB CRC64;
"A suppressor gene that enables Saccharomyces cerevisiae to grow without making sphingolipids encodes a protein that resembles an Escherichia coli fatty acyltransferase.";
J. Biol. Chem. 268:22156-22163(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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                                                                                                                                                                                                                                                                                                                                                                                         Urrestarazu L.A., Andre B., Vissers S.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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SEQUENCE FROM N.A.
MEDLINE=94012814; Pubmed=8408076;

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WIPFFGQLYWLTGNLLIDRNNRTKAHGTIAEVVNHFKKRRISIW--MFPEGTR----- 150
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PLSC_SALTY
ID _PLSC_SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "THE COMPLETE GROWE SEQUENCE OF ESCHETICHIA COLI K-12.";
Science 277:1453-1474(1997)
-!- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC
ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION. THIS ENZYME
CAN UTILIZE BITHER ACYL-COA OR ACYL-ACYL CARRIER PROTEIN AS THE
FATTY ACYL DONOR.
-!- CATALYTIC ACTIVITY: Acyl-COA + 1-acyl-sn-glycerol 3-phosphate.
-!- PATHWAY: De novo phospholipid biosynthesis; second step.
-!- PATHWAY: De novo phospholipid biosynthesis; second step.
-!- SUBCELLULAR LOCATION: Inner membrane-associated.
-!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP
acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Gregor J., Davis N.W., Kirkpatrick Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562,
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REMBL; M63491; AAA69186.1; -.

REMBL; AE000384; AAC76054.1; -.

REMBL; S20460; S20460.

RECGGENE; EG11377; plsC.

DR. InterPro; IPR004552; AGP acyltrn.

DR. Ffam; PF01553; Acyltransferase.

DR. SMART; SM00563; PlsC; 1.

DR. SMART; SM00563; PlsC; 1.

DR. TIGRFAMS; TIGR00530; AGP acyltrn; 1.

KW. Phospholipid biosynthesis; Transferase; Acyltransferase;

KW. Phospholipid biosynthesis; Transferase;

KW. Inner membrane; Formylation; Complete protecome.

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**Anth 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the Escherichia coli gene for 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC)."; Mol. Genet. 232:295-303(1992).
                                                                                                                                                                                                                                                                                                                                                                                                               [1] -
SEQUENCE FROM N.A., AND SEQUENCE OF 1-7.
MEDLINE=92212294; PubMed=1557036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acyltransferase family.
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hes 59; Conservative
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SEQUENCE FROM N.A.

SPECIES=S.typhi; STRAIN=CT18;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

A Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Cronin A., Davies P., Davies R.M., Hien T.T., Holroyd S., Jagels K.,

Rrogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitehead S., Barrell B.G.,

"Complete genome sequence of a multiple drug resistant Salmonella

enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21534948; PubMed=11677609; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFK
                          | ::: || | :|| | :|| | GLV------IVEMLPPIDVSQYGKDQVRELAAHCRSIMEQKIAELDKEVAE 238
                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP
acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES=S.typhimurium, STRAIN=LT2;
MEDLINE=92089025; PubMed=1751451;
Luttinger A.L., Springer A.L., Schmid M.B.;
"A cluster of genes that affects nucleoid segregation in Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                           GQPSVVHVHIKRHLMKELPDTD------EAVAQWCRDIFVAKDALLDKHMAE
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SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; Pubmed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 236-245 FROM N.A.
SPECIES=S.typhimurium; STRAIN=LT2;
Cong J., Schmid M.B.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                    STY3350 OR T3094
                                                                                                                                                                                                                                                                                                                                                                PLSC OR PARF OR STM3173 OR Salmonella typhimurium, and Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. 3:687-697(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=602, 601;
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SEQUENCE FROM N.A.
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1-12 -

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PLSC_LIMDO.
ID PLSC_LIMDO ST
AC Q42870; Q40120;
DT 15-DEC-1998 (Rel.
DT 15-DEC-1998 (Rel.
DT 28-FEB-2003 (Rel.
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                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVKVQIF--TDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SRG----RGLLPFKTGAFHAAIA---AGVPII----PVCVSNTSNKVNLNRLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 FLPVIGWSMWFSEYLFLER-SWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLL
                                        FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC ACID BY INCORPORATING ACYL MOISTY AT THE 2 POSITION. THIS ENZYME CAN UTILLIZE BITHER ACYL-COA OR ACYL-ACYL CARRIER PROTEIN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 GQPSVVHVHIKRHLMKELPDTD-----EAVAQWCRDIFVAKDALLDKHMAE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate = CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
PATHWAY: De novo phospholipid biosynthesis; second step.
SUBCELLULAR LOCATION: Inner membrane-associated.
SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Limnanthaceae, Limnanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                      EMBL; AE008845; AAA56678.1; -.
EMBL; AE008845; AAA56678.1; -.
EMBL; AL627277; CAD03005.1; -.
EMBL; AE57277; CAD03005.1; -.
EMBL; AE57277; CAD03005.1; -.
EMBL; AE582; B45582.
Stydene; SG10303; plsC.
InterPro; IPR004552; AGP acyltrn.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
TIGRFAMS; TIGR00530; AGP acyltrn; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%; Score 120; DB 1; Length 245; llarity 25.1%; Pred. No. 0.0034; Conservative 37; Mismatches 81; Indels E
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          and CT18.";
J. Bacteriol. 185:2330-2337(2003)
-!- FUNCTION: CONVERTS LYSOPHOSPH
                                                                                                                                                                                                                                                                                                               EMBL; M68936; AAA27181.1; -.
                                                                                                                                                                   acyltransferase family
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                                                                                 FATTY ACYL DONOR
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ID PLSC_LIMAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 VCFAIV--------LITAVAWGLIMVLLLPWPYMRIRLGNLYGHIIGGLVIWLYG
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                                                                                                                                                                                                                                                                                                           Lassner M.W., Levering C.K., Davies H.M.D., Knutzon D.S.,
Lassner M.W., Levering C.K., Davies H.M.D., Knutzon D.S.,
"Lysophosphatidic acid at the sn-2 position of triacylglycerol in
transgenic rapesed oil.",
Plant Physiol. 109:1389-1394(1995).
-!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic
acid by incorporating acyl moiety at the 2 position. This enzyme
uses eruccyl-CoA as an acyl donor.
-!- CATALYTIC ACTIVITY: Acyl-CoA + 1.acyl-sn-glycerol 3-phosphate =
CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
-!- PATHWAY: De novo phospholipid biosynthesis; second step.
-!- SIMBCELULAR LOCATION: Integral membrane protein (Potential).
-!- SIMBLARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77; Gaps
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TIGRFAMs; TIGR00530; AGP_acyltrn; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
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InterPro; IPR004552; AGP_acyltrn.
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Pfam; PF01553; Acyltransferase; 1.
                                                                                                                                                                                                                                                          MEDLINE=96106201; PubMed=8539298;
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281 AA;
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NCBI_TaxID=42439;
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MEDLINE=96046746; PubMed=7579178;

MEDLINE=96046746; PubMed=7579178;

MEDLINE=96046746; PubMed=7579178;

MEDLINE=96046746; PubMed=7579178;

MEDLINE=96046746; PubMed=7579178;

MEDLINE=96046746; PubMed=7579178;

MEDLINE=96046746; PubMed=7579178;

MEDLINE=96046746; PubMed=7579178;

Plant Mol. Brol. 29:267-278(1995)

L. Plant Mol. Biol. 29:267-278(1995)

L. FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic acid by incorporating acyl moiety at the 2 position. This enzyme uses erucoyl-CoA as an acyl donor.

CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate = CoA + 1,2-diacyl-sn-glycerol 3-phosphate.

COA + 1,2-diacyl-sn-glycerol 3-phosphate.

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

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COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-phosphate |

COA + 1,2-diacyl-sn-glycerol 3-pho
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                                                                                                Limnanthes douglasii (Douglas's meadowfoam).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Limnanthaceae; Limnanthes.
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                   MEDIINE=96028122; Pubmed=7588719;
Hanke C., Wolter F.P., Coleman J., Peterek G., Frentzen M.;
"A plant acyltransferase involved in triacylglycerol biosynthesis
complements an Escherichia coli sn-1-acylglycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.1%; Score 118.5; DB 1; Length 281; Best Local Similarity 21.7%; Pred. No. 0.0055; Matches 56; Conservative 46; Mismatches 79; Indels 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X83266; CAA58239.1; ...
EMBL; Z46836; CAA58239.1; ...
PIR; S60477; S60477.
InterPro; IPR002123; Acyltransferase.
InterPro; IPR004552; AGP acyltrn.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
TIGRFAMS; TIGR00530; AGP acyltrn; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I -> V (IN REF. 2).
R -> G (IN REF. 2).
V -> I (IN REF. 2).
N -> K (IN REF. 2).
W; 9C880BD9E492EE2A CRC64;
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POTENTIAL.
POTENTIAL.
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Eur. J. Biochem. 232:806-810(1995)
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281 AA;
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SEQUENCE FROM N.A.
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NCBI_TaxID=28973;
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arch completed: July 7, 2004, 13:40:19 b time : 20 secs

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2004, 13:37:33 ; Search time 21 Seconds (without alignments) 1726.867 Million cell updates/sec

Title:
Perfect score: 1935
Sequence: 1 MAIAAAAVVVPLGLLFFASG......QSERSNPAKIVPAKSKNKGS 377
Scoring table: BLOSUM62

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 78:\*
1: Dirl:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	le 1-acyl-	1-acyl-g	ical	glyd	g,	i,		tica		ica	ical	membran	cal pro	polynu			probable endonucle	probable polynucle	probable acyltrans	poly		probable sn2-acylg	1-acylg	1-acylglycerol-3-p	ycerol-	obable 1-acylgl	1-acylglycerol-3-p	/lglycerol-3-	hypothetical prote
CI CI	98	S5264	D9655	T0675	T0793	B9678	T4046	T3191	84590	T3405	T2268	S5464	T2599	B8354	S4080	A9122	G8607	B8358	AI095	D823	T1536	A486	B4558	S2046	AE088	T501	S6047	D64	T2060
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RESULT 2

1-acyl-sn-glycerol 1-acyl-sn-glycerol 1-acylglycerol-3-p	hypothetical prote probable acyltrans probable 1-acylgly 1-acyl-sn-glycerol	<pre>1-acylglycerol-3-p 1-acylglycerol-3-p hypothetical prote transcription elon</pre>	transcription elon 2-acylglycerophosp probable 1-acylgly	1-acylglycerol-3-p conserved hypothet
F85961 F91116 AC0083	G97788 A83645 B71706 G81013	T24610 A81957 G72223 B86583	C72040 E70476 C82067	JC5639 B70078
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## ALIGNMENTS

RESULT 1 S60478 probable 1-acy C; Species: Lim C; Dates 10-mar C; Accession: S R; Brown, A.P.; Plant Mol. Bio A; Title: Ident A; Reference nucl A; Notes: nucl A; Note: the nucl A; Note: the nucl C; Superfamily: Query Match Best Local S	RESULT 1 S60478 probable 1-acyl-sn-glycerol-3-phosphate acyltransferase - Limnanthes douglasii C;Species: Limnanthes douglasii C;Species: Limnanthes douglasii C;Species: Limnanthes douglasii C;Species: Limnanthes douglasii C;Species: Limnanthes douglasii C;Species: Limnanthes douglasii C;Species: Limnanthes douglasii C;Date: 19-Mar-1997 #sequence _revision 19-Mar-1997 #text_change 17-Mar-2000 C;Actors in 29, 267-278, 1995 A;Title: Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-phosphate acyltra: A;Reference number: S60477; MUID:96046746; PMID:7579178 A;Accession: S60478 A;Accession: S60478 A;Accession: S60478 A;Accession: S60478 A;Accession: S60478 A;Accession: S60478 A;Accession: S60478 A;Cross-references: EMBL:Z48730; NID:gl067137; PIDN:CAA88620.1; PID:gl067138 A;Cross-references: EMBL:Z48730; NID:gl067137; PIDN:CAA88620.1; PID:gl067138 A;Cross-references: EMBL:Z48730; NID:gl067137; PIDN:CAA88620.1; PID:gl067138 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995 C;Superfamily: probable membrane protein YBR042c Query Match Best Local Similarity 77.08; Pred No. 1.5e-124; Best Local Similarity 77.08; Pred No. 1.5e-124;
Marches Qy Db	MAIDAAAFIVPISLLFFMSGLVVNFIQAVFYVLVRPISKDIYRRINTVAELLWLELVWL 60 MAIDAAAFIVPISLLFFMSGLVVNFIQAVFYVLVRPISKDIYRRINTLVAELLWLELVWV 60
oy op	61 IDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK 120 
 δ Pa	121 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180 
Qy	181 LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHWRSFVPAIYDVTVAIPKSSPAPTMLRL 240 
Qy	241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300  : :       :
oy Dp	301 RPIXSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360   :  :  :  :
Qy	361 RSNPAK 366           361 HSTPAK 366

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Local Similarity 61.3%
nes 228; Conservative
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                                                                                             Similarity
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A;Gene: F11M15.12
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Matches 228; (
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002
C;Accession: D96550
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anture 10, 200
A;Authors: Hunter, J.E.; Denkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96550
A;Estuts: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <STO>
                                                                                                                                    sn-gly
   probable 1-acyl-glycerol-3-phosphate acyltransferase - maize C; Species: Zea mays (maize) C; Species: Zea mays (maize) C; Species: Zea mays (maize) C; Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-May-2000 C; Accession: S52645 R; Brown, A.P.; Coleman, J.; Tommey, A.M.; Watson, M.D.; Slabas, A.R. Plant Mol. Biol. 26, 211-223, 1994 A; Title: Isolation and characterisation of a maize cDNA that complements a 1-acyl shart acyltransferases. A; Reference number: S52645; MUID:95035993; PMID:7948871 A; Reference number: S52645 A; Reference number: S52645 A; Residues: 1-374 <BRO> A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-374 <BRO> A; Cross-references: EMBL:Z29518; NID:g575959; PIDN:CAA82638.1; PID:g575960 C; Superfamily: probable membrane protein YBR042c
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                                                                                                                                                                                                                                                                                                                         tch 75.0%; Score 1450.5; DB 2; Length al Similarity 70.7%; Pred. No. 1.4e-118; 265; Conservative 51; Mismatches 58; Indels
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probable glycerol-3-phosphate O-acyltransferase (BC 2.3.1.15) - Arabidopsis thaliana N;Alternate names: protein F15B8.160 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-May-2000 C;Accession: T06755 R;Quetier, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Salanoubat, M.; Mewes, submitted to the Protein Sequence Database, April 1999
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                                                                                 Length 376;
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A;Molecule type: DNA
A;Residues: 1-310 <QUE>
A;Cross-references: EMBL:AL049660; GSPDB:GN00061; ATSP:F15B8.160
A;Experimental source: cultivar Columbia; BAC clone F15B8
                                                                                                                                     Indels
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A;Introns: 26/3; 46/3; 72/3; 125/3; 167/3; 198/3; 227/3
C;Superfamily: probable membrane protein YBR042c
C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                             66.0%; Score 1277; DB 2; ilarity 62.3%; Pred. No. 1.8e-103; Conservative 62; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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A, Map position: 1
C; Superfamily: probable membrane protein YBR042c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.0%; Score 1161.5;
61.3%; Pred. No. 1.6e
live 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VIAAAVIVPLGLLFFISGLAVNLF----
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Db Db Db Db Db Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy	Db 43 KFLPVIGWSWWFSEYLFLERNWAKDESTLKSGLORLSDFPRFFWLALFVEGTRFTEAKLK  Qy 183 AAQEYAASSELPIPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTWLRLFR  Db 103 AAQEYAASSELPIPRNVLIPRTKGFVSAVSHMRSFVPAIYDWTVTIPKTSPPTWLRLFR  QY 243 GQPSVVHVHIKEHLMKELDDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTGRP  Db 163 GQPSVVHVHIKCHSWKDLPESDDAIAQWCRDFVAKDALLDKHMAEGTFSDOELQDTGRP  QY 303 IKSLAVYLSWACTLVAGSVKFCWSSLLSSWKGVAKDALLDKHIAADTFPGQOEQNIGRP  QY 303 IKSLAVYLSWACTLVAGSVKFCWSSLLSSWKGVARFAFGLAVYTALMOILIOFSGSERS  QY 365 NPAKIVPAKSKN 374  Db 223 IKSLAVYLSWACTLGAIKFLHWAQLFSSWKGITISALGLGIITLCWQILLRSSQSERS  QY 363 NPAKIVPAKSKN 374  Db 283 TPAKVVPAKFKD 294  RESULT 5  TO7936  Qy 363 NPAKIVPAKSKN 374	AKLK 102  **LEK 242           **LEK 162           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242           **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242                 **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242               **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242             **LEK 242           **LEK 242           **LEK 242           **LEK 242
C; Superfam C; Keywords	le membrane protein YBR042c ferase; coenzyme A	
Query Ma Best Loc Matches	y Match Local Similarity 61.4%; Pred. No. 4.5e-93; hes 227; Conservative 33; Mismatches 31; Indels 79;	a <u>p</u> s 1;
Qy Dp	5 AAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWL     :            4 AAAVIVPLGILFFISGLVVNLL	IDWW 64
ογ	65 AGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKS	SSKF 124
QQ	26QRSGCLGSALAVMKKS	  SSKF 44
, q <sub>Q</sub>	125 LEVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAA 	LLAA 184      LKAA 104
Qy Db	185 QEYATSIGLPVPRNVLIPRIKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFKGQ 	FKGQ 244       KGQ 164
ò	ĽΩ	RPIK 304
		 RPIK 224
οχ	305 SLLVVISWACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNP	36
qa	225 SLAVVLSWACLITLGAMKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQSER	RSTP 284
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hypothetical protein F9EI0.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001
C;Accession: B96780
C;Accession: B96780
Cin, C.W.; Chung, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hudhes, B.; Hudzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.A.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96780
A;Cacssion: B96780
A;Cacssion: B96780
A;Cacssion: B96780
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A;Cacssi 60 LIDWWAGVKVOIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAORSGCLGSTLAVMK 119 KLLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLR 239 120 KSSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIORLSDFPLPFWLALFVEGTRFTQA 179 240 LFKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDT 299 59 16 9 VVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRI-----NRVVAEL----LWLEL-VW Query Match 21.4%; Score 414; DB 2; Length 393; Best Local Similarity 34.2%; Pred. No. 3.1e-28; Matches 106; Conservative 52; Mismatches 132; Indels 20; Gaps 300 GRPIKSLLVV 309 180 77  $\delta$ d g ò В δ 임 상 임 ò ð

probable acetyltransferase protein - fission yeast (Schizosaccharomyces pombe)
c;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 01-Mar-2002
C;Accession: T40466
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
submitted to the EMBL Data Library, November 1998
A;Recence number: Z21931
A;Accession: T40466
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recission: T40466
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-350 <LYNA>
A;Residues: 1-350 <LYNA>
A;Residues: 1-350 <LYNA>
A;Cross-references: EMBL:AL034382; PIDN:CAA22289.1; GSPDB:GN00067; SPDB:SPBC428.14
A;Gene: SPDB:SPBC428.14
A;Map position: 2
C;Superfamily: probable membrane protein YBR042c

307 -RPEEELSVL 315

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hypothetical protein F28B3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34057
B;Geisel, C.; Kramer, J.; Smith, A.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F28B3.
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C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31913
R;Blanchard, M.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid T05H4.
A;Reference number: Z21097
A;Accession: T31913
A;Reference number: Z21097
A;Accession: T31913
A;Residues: 1-344 <BLA>
A;Accession: T31913
A;Especule type: DNA
A;Residues: 1-344 <BLA>
A;Cross-references: EMBL:AF016452; PIDN:AAB66008.1; GSPDB:GN00023; CESP:T05H4.1
A;Experimental source: strain Bristol N2; clone T05H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                          83 KEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFLER 142
                                                                                                                                                                                 SWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAAQEYATSTGLPVPRNVLIP 202
                                                                                                                                                                                                                                                                                                                                       HLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKSLLVVIS--- 311
                                                                                                                                                                                                                                                                                                                                                                                                                273 FPISBIPTEBDQFTDWLYQRWYEKDKLIDTLLETGNFPGPKKLHTTVRLKHRLEILSLFS 332
                                                                                                                                                                                                                                                                                                             RIKGFVSAVSHMRSFVPAIYDVTVAIPKSSP-----APTMLRL-FKGQP-SVVHVHIKR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NFRVTGDLIERDEPAILIMMHRTRLDWLFSWNALYKMDPWLLTTEKISLKAPLKK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 FIDHETFRIMG----KEHALVISNHRSDIDWLVGWVSAQRSG--CLGSTLAVMKKSSKF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 QEYATSIGLPVPRNVLIPRIKGFVSAVSHMR--SFVPAIYDVIVAIPKSSPAPIMLRLFK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 DAFADKNGLPRYEYVLHPRTTGFKFLMBLMKKENYIKYVYDLTIAY-SGTIVDTBAKLLA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 GQ-PSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDK----HMAEGTFSDQEL 296
                                                                                 82
                                                                                                    |:| | | : | : | : | : | : | : | 36 VNKELYNKYIAFTKSFAGILFTALVQL---FSPTPVTLTYDPELRNLFYLDRNGCLETIA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 LPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LLFFASGLLVNLIQAICYVVVRPVSKSLYRR-INRVVAELLWLEL-VWLIDWWAGVKVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
    Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.8%; Score 287; DB 2; Length 344; Best Local Similarity 26.7%; Pred. No. 3e-17; Matches 92; Conservative 64; Mismatches 157; Indels :
                                                                            37 VSKSLYRR---INRVVAELLWLELVWLIDWWAGVKVQIFTDHETFRL-
                                         Indels
16.0%; Score 310.5; DB 2; ilarity 27.1%; Pred. No. 2.8e-19; Conservative 62; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:T05H4.1
A;Map position: 5
A;Introns: 55/3; 212/1; 243/3; 298/3
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                   Similarity
                                      84;
 Query Match
Best Local S
Matches 84
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probable membrane protein YBR042c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YBR0412
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: 845900
R;Andre, B.; Cziegluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
Submitted to the Protein Sequence Database, August 1994
A;Reference number: 845893
A;Accession: 845800
A;Recence number: 845893
A;Accession: 845800
A;Recence number: 845893
A;Accession: 845800
A;Recence number: 82880
A;Cross-references: EMBL:235911; NID:9536265; PIDN:CAA84984.1; PID:9536266; GSPDB:GN0000
A;Cross-references: SGD:S0000246
A;Gene: MIPS:YBR042c
A;Generics:
A;Gene: MIPS:YBR042c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 LIDWWAGVKVQIFTDHE----TF-----RLMG--KEHALVISNHRSDIDWLVGWVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 ------QRLSD------FPLPFWLALFVEGTRFTQAKLLAAQEYATSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VVVP-LGLLFFASGLLVNLIQAICYVVVRPVSKSLY-----RRINRVVAELLWLELV-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVVHVHIKRHIMKELPDTDE-AVAQWCRDIFVAKDALLDKHMAEGTF-SDQE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.0%; Score 271; DB 2; Length 397; Best Local Similarity 24.6%; Pred. No. 9.2e-16; Matches 87; Conservative 72; Mismatches 122; Indels '
297 QDTGRPIKSLLVVISW--ACLVVAGSVKFLQWSSLLSSWKGVAFS 339
                                                                          298 PETTTGIGYYVAFAFWVLASLIWMGAIYSLLWVKVINRFYGDCYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193
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A;Molecule type: DNA
A;Residues: 1-918 <GEI>
A;Cross-references: EMBL:AF003136; PIDN:AAB93636.1; GSPDB:GN00019; CESP:F28B3.5
A;Experimental source: strain Bristol N2; clone F28B3
C;Genetics:
A;Gene: CESP:F28B3.5
A;Gene: CESP:F28B3.5
A;Map position: 1
A;Introns: 85/3; 129/3; 235/3; 418/2; 482/3; 532/3; 736/3; 829/3; 850/2 hypothetical protein F55All.5 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Accession: T22689
R;Kershaw, J.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19600
A;Reference number: Z19600
A;Accession: T22689
A;Accession: T22689
A;Accession: T22689
A;Accession: T22689
A;Cross-references: EMBL:Z72511; PIDN:CAA96659.1; GSPDB:GN00023; CESP:F55All.5
A;Cross-references: EMBL:Z72511; PIDN:CAA96659.1; GSPDB:GN00023; CESP:F55All.5
A;Genetics:
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A;Gene 11; 60 LIDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSG--CLGSTLAV 117 : | ::|:| || || || || || || : :: || EWITLESSEVIRFKNUHFYRFIKIQK 196 645 220 | | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : VAELLWLELVWLIDWWAGVKVQIF-TDHETFRLMGK-EHALVISNHRSDIDWLVGWVSAQ 106 107 RSGCLGSTLA---VMKKSSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPL 163 ---AIPKSSPAPTMLRLFKG--OPSVVHVHIKR 254 1 MAIAAAAVVVPLGLLF-----YRSGLLVNLIQAICYVVVRPVSKSL-----YRRINRV 48 118 MKKSSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFT PFWLALFVEGTRFTQAK---LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPA 12.9%; Score 250; DB 2; Length 439; 25.1%; Pred. No. 7.1e-14; iive 54; Mismatches 106; Indels 34; Gaps Gaps 60; Length 918; Query Match 13.9%; Score 269; DB 2; Length 91 Best Local Similarity 26.3%; Pred. No. 4.2e-15; Matches 88; Conservative 67; Mismatches 119; Indels A;Map position: 5 A;Introns: 19/3; 52/2; 176/1; 222/3; 260/2; 327/1; 342/1 OAKLLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMR---: |:| : | : | : | : | : | : | IDIDEVPKAKLELRTWTIERFTKKERIIDEFYSE 858 255 HLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAE 288 Query Match
Best Local Similarity 25.1%
Matches 65; Conservative 221 IYDVTV-49 539 646 306 765 825 164 g <del>Q</del> ò d ઠ 셤  $\delta$ 셤 ò g  $\delta$ g  $\overset{\circ}{\circ}$ 8 õ 셤 à

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Stafet membrane protein VDR018c - yeast (Saccharomyces cerevisiae)
Nr.Alternate names: Hypothetical protein D3246; hypothetical protein P2F396; hypothetical C.Species: Saccharomyces carevisiae
C.Species: Saccharomyces carevisiae
C.Species: Saccharomyces carevisiae
C.Species: Saccharomyces carevisiae
C.Species: Saccharomyces carevisiae
C.Species: D424: S65425; 65631; 872166
R.Dednan, K.; Brown, D. Hamlyn, N.; B72166.
A.Reference number: S54638
A.Reference number: S54638
A.Reference: Stafet D429770; NID:8840867; PIDN:CAA89843.1; PID:9840871
A.Rocession: S54641
A.Rocession: S54641
A.Rocession: S6441
A.Rocession: S6345
A.Reference number: S6346
A.Reference number: S6346
A.Reference number: S6346
A.Residues: 1-396
A.Rocession: S6345
A.Rocession: S6345
A.Rocession: S6345
A.Rocession: S6346
A.Rocession: S6346
A.Rocession: S6346
A.Rocession: S6346
A.Rocession: S6381
A.Rocession: S6782
A.Rocession: S67831
A.Reference number: S6782
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A;Molecule type: DNA
A;Residues: 1-396 <EIW>
A;Cross-references: EMBL:X95966; NID:g1216215; PIDN:CAA65210.1; PID:g1216225
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || | : | | : | | : | | : | | : | | : | | : | | : | | ETSRPLKNSSNAKPCFRFKDRAIIIANHQMYADWIYLWWLSFVSNLGGNVYIILKKALQY 149
                                  197 IIILBEYVEYIYDITIAYPYNIVQSEIDLVLKGASPREVHFHIRKIPISQVPLNEQDASR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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----SFVPALYDVTVALPKSSPAPTMLRLFKG-QPSVVHVHIKRHLMKELPDTDEAVAQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 ETFRLMG------KEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 FISGSLSIVVFQICLQVLLPWSKIRFQNGINQSKKAFIVL-LCMILNMVAPSSLNV--TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Keywords: transmembrane protein;
;27-43/Domain: transmembrane #status predicted <TMl>
;69-85/Domain: transmembrane #status predicted <TM2>
;376-392/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: probable membrane protein YBR042c
                                                                                                                                                                                                                             275
                                                                                                                                                    288
                                                                                                                                                                                                    257 WLTDRWTIKEQLLHDFYSE
                                                                                                                                                       WCRDIFVAKDALLDKHMAE
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Best Local Similarity 25.8'
Matches 85; Conservative
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A; Note: YDR018c
                                                                                                                                                       270
   216
                                                  QQ
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Qy	125 LPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLP 164	- X	R;Stover, C.K
qq	150 IPLLGFGMRNFKFIFLSRNWQKDEKALTNSLVSMDLNARCKGPLTNYKSCYSKTNESIAA 209		- 00 y
QY	165 FWLALFVEGTRFTQAKLLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAI 221	A A S	A;Title: Comp
Dp	FPEGTNLSLKTREKSBAFCQRAHLDHVQL-RHLL	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ccession:
δ	AIPKSSPAPT	N K I	catus: pre olecule ty
qq	269 YDVTIGYSPALRTEYVGTKFTLKKIFLMGVYPEKVDFYIREFRVNEIPLQDDEVFFN 325	A A	esidues: ross-refe
Qy	FVAKDALL	M O	xperimenta enetics:
qa	326 WLLGVWKEKDQLLEDYYNTGQFKSNAKND 354	A;0,0	A;Gene: PA083 C;Superfamily C;Keywords: n
RESULT	13	O n	Query Match
hypothe	tical protein ZK40.1 - Caenorhabditis elegans	<u>-</u>	Matches 7
C;Date:	15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 sion. 705098	δ —	13
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A; Acces	sion: Tables to the form of th	QC	69
A;Molec		λο ^	112
A, Cross	incs: 1-523 SERA; i-references: BMBL:U64839; PIDN:AAB04844.1; GSPDB:GN00023; CESP:ZK40.1 imental convo. strain Bristol NO. Jone 7040	qo	113
C;Genet		ð	161
A; Map F A; Intro	A; mono	qa	173
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ζ	287 AEGTFSDQELQDT 299	, w	ao, G.J.;
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C;Speci C;Date:	Sep-2000 #text change 02-Mar-2001		; Rose, D.c.
C;Acces		A,T	itle·

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plete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonumber: A82950; MUID:20437337; PMID:10984043
B83541
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-ype: DNA
1-304 <STO>
erences: GB:AE004518; GB:AE004091; NID:g9946725; PIDN:AAG04223.1; GSPDB:GN001
eal source: strain PAO1
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nucleotide sequence was submitted to the EMBL Data Library, October 1993
Pogliano, J.; Sarkar, N.
Acad. Sci. U.S.A. 93, 11580-11585, 1996
ntification of the coding region for a second poly(A) polymerase in Escheric number: JC6149; MUID:97030237; PMID:8876178
K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bruan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Olson, M.V.
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A; Molecule type: DNA
A; Residues: 1-310 < CAO>
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title The complete genome sequence of Escherichia coli K-12
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Y: Escherichia coli polynucleotide adenylyltransferase II yihG
nucleotidyltransferase
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A, Reference A, Accession	A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B65191	
A; Molecule type: DNA	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA	
A; Experimen	A, Kristiques: 1-310 central, AB. U00096; NID: g2367318; PIDN: AAC76860.1; PID: g1790293; A, Experimental source: strain K-12, substrain MG1655	Ē
C;Genetics: A;Gene: yinG C;Superfamil C;Keywords:	C;Genetics: A;Gene: yihG C;Superfamily: Escherichia coli polynucleotide adenylyltransferase II yihG C;Keywords: nucleotidyltransferase	
Query Mat Best Loca Matches	Query Match  7.6%; Score 148; DB 2; Length 310;  Best Local Similarity 21.6%; Pred. No. 3.4e-05;  Matches 71; Conservative 58; Mismatches 115; Indels 84; Gaps 14;	
<i>\$</i> 5	6 AAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLEL 57	
qa	15 AAITLLSIVLTILVTIFCSVPIIIAGIVKLLLPVPVIWRKVSRFCDFMMYC 66	
٥٨	58 VWLIDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGC 110	
Db	57WCEGLAVLLHLNPHLQWEVHGLEGLSKKNWYLLICNHRSWADIVVLCVLFRKH 119	
Qy 1	111 LGSTLAVMKKSSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLS 159	
Db 1	120 IPMNKYFLKQQLAWVPFLGLACWSLDMPFMKRYSRAYLLRHPERRGKDVETTRRSCEK 177	
Qy 1	160 DFPL-PFWLALFVEGTRFTQAKLLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFV 218	
Db 1	78 -FRLHPITIVNFVEGSRFTQEKHQQTHSTFQNLLPPKAAGIAMALNVLGKQF 228	
ΟΥ 2	219 PAIYDVTVAIPKSSPAPTMLRLFKGQPSVVHVHIKRHLMKE 259	
Db 2	229 DKLINVTLCYPDNNRQP-FFDMLSGKLTRIVVHVDLQPIADBLHGDYINDKSFKRHFQ 285	
Qy 2	260 LPDTDEAVAQWCRDIFVAKDALLDKHMA 287	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 278313,	Sequence 47952, A		Sequence 57801, A	Sequence 51954, A	Sequence 278291,	Sequence 4, Appli	Sequence 67316, A	Sequence 66105, A	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 130474,
ΩI	US-10-424-599-278313	US-10-425-114-47952	US-10-424-599-210085	US-10-425-114-57801	US-10-425-114-51954	US-10-424-599-278291	US-08-818-581B-4	US-10-425-114-67316	US-10-425-114-66105	US-09-970-989-5	US-10-667-494-5	US-10-667-462-5	US-10-667-464-5	US-08-818-581B-5	US-10-437-963-130474
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# ALIGNMENTS

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Sequence 278313, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Clone ID: PAT_MRT3847_9333C.1.pep US-10-424-599-278313
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366 KIVPA-KSKN 374
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US-10-424-599-210085
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 47952
                                               181 LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
                                                                                                                                                                                                                            301 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360
                                                                                                               FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALJDKHMAEGTFSDQELQDTG 300
                                                                                                                                                                                                    301 RPIKSLLVVISWACLVVAGSVKFLQMSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSF 360
                      LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
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                                                                                                                                                        241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300
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US-10-425-114-47952
                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-47952; Sequence 47952, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            361 RSNPAKIVPAKSKNKGS 377
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Best Local Similarity 100.(
Matches 342; Conservative
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Sequence 57801, Application US/10425114;
Sequence 57801, Application US/10425114;
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 57801
Sequence 210085, Application US/10424599

Sequence 210085, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 210085

LENGTH: 419
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241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300
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Sequence 51954, Application US/10425114

Sequence 51954, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, US/E E

APPLICANT: Tabaska, US/E E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 51954

LENGTH: 399

LENGTH: 399

LENGTH: 399
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                                                                                                                                                                                                           GVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFL
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                                                                                                Query Match 89.5%; Score 1731; DB 12; Best Local Similarity 89.4%; Pred. No. 2.9e-173; Matches 330; Conservative 17; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: 700844230_FLI.pep
US-10-425-114-51954

; LENGTH: 406
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701127504_FLI.pep
US-10-425-114-57801
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KVAPAKSKN 394
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RESULT 6
US-10-424-599-278291

i Sequence 278291, Application US/10424599

i Publication No. US20040031072A1

i GENERAL INFORMATION:

i APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

i APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 278291

LENGTH: 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180
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                                                                               EYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPALYDVTVALPKSSPAPTMLRLFKGQP
                                                                                                                                                                                     198 EYAASAGLPVPRNVLIPRTKGFVSAVNHMRSFVPAIYDVTVAIPKSSPAPTMLRLFRGKS
                                                                                                                                                                                                                                            246 SVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKS
GVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKFL
                          58;
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Best Local Similarity 84.4%; Pred. No. 9.2e-159;
Matches 318; Conservative 0; Mismatches 1; Indels 58.
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US-10-424-599-278291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(319)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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378 KVAPTKKSKN 387
                                                                                                                                                                                                                                                                                                                                                                                                              KIVPA-KSKN 374
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ORGANISM: Glycine max
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Sequence 67316, Application US/10425114

Fublication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen E

APPLICANT: Screen E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 67316

LENGTH: 425
                                                                                       301 RPIKSLLVVISWACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTALMOILIQFSOSE 360
                                                                                                                        301 RPMKSLVVVVSWMCLLCLGLVKFLQWSALLSSWKGMMITTFVLGIVTALMHILIRSSQSE 360
SSKFLPVIGWSMWPSBYLFLERSWAKDESTLKSGIQRLSDPPLPFWLALFVEGTRFTQAK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: LIB4765-008-H3_FLI.pep
US-10-425-114-67316
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US-10-425-114-66105
; Sequence 66105, Application US/10425114
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ORGANISM: Zea mays
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US-10-425-114-67316
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ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/00306
FILING DATE: March 14, 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 9502468.3
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: GB 9502468.3
FILING DATE: 09-FEB-1995
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 377;
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                                                                                                                                                                                                                                            US-08-818-581B-4
; Sequence 4, Application US/08818581B
; Publication No. US20020007499A1
; GENERAL INFORMATION:
; APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: BROWN, Adrian Paul
; APPLICANT: BROWN, Johannes Theodorus Maria
ITILE OF INVENTION: 2-ACYLTRANSFERASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 78.7%; Score 1523; DB 8; Best Local Similarity 77.3%; Pred. No. 2.2e-151; Matches 283; Conservative 43; Mismatches 40;
                                                                                                                                                                                          361 RSNPAKIVPAKSKNKGS 377
                  FKGQPSVVHVH--
                                                                                                                                  252
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66105
LENGTH: 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDWWAGVKYQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09970989
; Sequence 5, Application US/09970989
; Patent No. US20020156262A1
; GENERAL INFORMATION:
    APPLICANT: LEUNG, David W.
    APPLICANT: HOLLENBACK, David
    TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/970,989
; CURRENT FILING DATE: 2001-10-05
; CURRENT FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVABLLWLBLVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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Best Local Similarity 70.9%; Pred. No. 8.7e-144;
Matches 266; Conservative 50; Mismatches 58; Indels 1;
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: LIB4315-045-D9_FLI.pep
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Publication No. US2004003488A1
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                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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; Sequence 5, Application US/10667494
; Publication No. US20040043465A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: HOLLENBACK, DAVID
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0275
; CURRENT APPLICATION NUMBER: US/10/667,494
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/09/970,989A
; PRIOR APPLICATION NUMBER: 09/215,252
; PRIOR APPLICATION NUMBER: 09/215,252
; PRIOR PILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO S: 45
; SEQ ID NO S: 45
; SEQ ID NO S: 45
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                                                          121 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK
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75.0%; Score 1450.5; DB 9; Length 374; 70.7%; Pred. No. 9.4e-144; ive 51; Mismatches 58; Indels 1;

Query Match Best Local Similarity 70.74 Matches 265; Conservative

; SEQ ID NO 5 ; LENGTH: 374 ; TYPE: PRT ; ORGANISM: Maize US-09-970-989-5

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301 RPIKSLLVVISWACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360
                                                       241 LKGQSSVIHVRMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
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                                                                                                                                                                                         US-10-667-464-5

1 Sequence 5, Application US/10667464

2 Publication No. US20040086996A1

3 GENERAL INFORMATION:

APPLICANT: LEUNG, DAVID W.

APPLICANT: HOLLENBACK, DAVID

TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

FILE REFERENCE: 077319/0275

CURRENT APPLICATION NUMBER: US/10/667,464

CURRENT FILING DATE: 2003-09-23

PRIOR APPLICATION NUMBER: US/09/970,989

PRIOR FILING DATE: 1098-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

SPRIOR FILING DATE: 1998-12-18

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                           360 RSSSARAARNRVKKE 374
                                                                                                    361 RSNPAKIVPAKSKNK 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Zea mays
US-10-667-464-5
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                 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSF 360
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Bublication No. US20040082049A1

GENERAL INFORMATION:

APPLICANT: LEUNG, DAVID W.

APPLICANT: HOLLENBACK, DAVID

ITILE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

FILE REFERENCE: 077319/0273

CURRENT FILING DATE: 2003-09-23

PRIOR APPLICATION NUMBER: US/09/970,989A

PRIOR APPLICATION NUMBER: US/09/970,989A

PRIOR FILING DATE: 1998-12-18

PRIOR APPLICATION NUMBER: 08/618,651

PRIOR APPLICATION NUMBER: 08/618,651

PRIOR APPLICATION NUMBER: 08/618,651

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 55
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Best Local Similarity 70.7%; Pred. No. 9.4e-144;
Matches 265; Conservative 51; Mismatches 58;
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; ORGANISM: Zea mays
US-10-667-462-5
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Publication No. US20020007499A1
GENERAL INFORMATION:
APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: BROWN, Adrian Publ
APPLICANT: BROWN, Adrian Publ
APPLICANT: BROWN, Johannes Theodorus Maria
APPLICANT: KROON, Johannes Theodorus Maria
TITLE OF INVENTION: 2-ACYLTRANSFERASE
NUMBER OF SEQUENCES: 13
CORRESSONDENCE ADDRESS:
ADDRESSEE: Cooper & Lunham LLP
STREET: 1185 Avenue of the Americas
COUNTRY: New York
STATE: New York
COUNTRY: US
ZIR: 10036
COMPUTER: EPLOPY disk
COUNTRY: US
COMPUTER: EPLOPY disk
COUNTRY: US
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,581B
FILING DATE: WO PCT/GB96/00306
FILING DATE: US-FEB-1996
APPLICATION NUMBER: US 9502468.3
FILING DATE: US-FEB-1996
APPLICATION NUMBER: US-FEB-1996
APPLICATION NUMBER: US-FEB-1996
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APPLICATION NUMBER: US-FEB-
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US-10-437-963-130474

US-10-437-963-130474

J Sequence 130474, Application US/10437963

J Sequence 130474, Application US/10437963

J Sequence 130474, Application US/10437963

J GENERAL INFORMATION:

J APPLICANT: Exousing Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

ITILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules

APPLICANT: Li, Ping

ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)8

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 130474

LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 74.3%; Score 1438.5; DB 16; Length 374; Best Local Similarity 72.1%; Pred. No. 1.7e-142; Matches 264; Conservative 46; Mismatches 55; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Oryza sativa
FEATURE:
CHER INFORMATION: Clone ID: PAT_MRT4530_32632C.1.pep
US-10-437-963-130474
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

(without alignments)
846.217 Million cell updates/sec 7, 2004, 13:38:43 ; Search time 23 Seconds OM protein - protein search, using sw model July Run on:

1 MAIAAAAVVVPLGLLFFASG.....QSERSNPAKIVPAKSKNKGS 377 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-914-098-56 1935 Scoring table: Perfect score: Sequence:

Total number of hits satisfying chosen parameters:

389414 seqs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2\_6/ptodata/2/jaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/jaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/jaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/jaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/jaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/jaa/PCTUS\_COMB.pep:\* Issued Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	equence 4,	equence 2,	Seguence 6, Appli	equence 2,	quence 6,	equence 2,	eguence 6,	equence 5,	equence 5,	equence 5,	equence 7,	equence 7,	equence 7,	ý	equence 13,	13,	equence 17,	equence 17,	15,	equence 15,	equence 4,	equence 4,	equence 4,	equence 5,	equence 5,	equence 5,	e 74
ID	-81	4-267-	-08-454-26	-319-	-08-941-319-	-035-098-	35-098-	-215-252-	-09-970-989A-	-818-581B	-08-454-267	-08-941-319-	5-09	-08-818-581B	-09-215-252-1	-09-970-989A-	-09-215-2	-970-989A-	-09-215-25	-09-970-989A-	-966-30	-09-338-90	-09-218-207-	-966-30	7-	-218-207	US-09-338-907-74
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61 IDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK 120

1 MAIAAAAVVVPLGILFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWL

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Sequence 74, Appl Sequence 70, Appl	~ <del>4</del>	134	127	equence 135	equence 128	equence 128	equence 136	equence 136	equence 294	equence 3826, A	equence 5730	equence 22552,	Sequence 133, App
US-09-218-207-74 US-09-338-907-70	US-09-218-207-70 US-09-338-907-134	US-09-218-207-134 US-09-338-907-127	-09-218-207-1	-09-218-207-13		US-09-218-207-128	US-09-338-907-136	US-09-218-207-136	-991A-29	US-09-540-236-3826	US-09-328-352-5730	US-09-252-991A-22552	US-09-338-907-133
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## ALIGNMENTS

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 10036
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,581B
FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: WO PCT/GB96/00306
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: GB 9502468.3
FILING DATE: 09-FEB-1995
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TOWATH: 377 amino acids
                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: BROWN, Adrian Paul
APPLICANT: BROUGH, Clare Louise
APPLICANT: KROON, Johannes Theodorus Maria
TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT
ITTLE OF INVENTION: 2-ACYLTRANSFERASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
; Sequence 4, Application US/08818581B ; Patent No. 6583340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.3
Matches 283; Conservative
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MOLECULE TYPE: protein
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Mon Jul 12 10:08:46 2004

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61 IDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK 120
                                                    61 VDWWAGVKVQLHADEETYRSMGKEHALIISNHRSDIDWLIGWILAQRSGCLGSTLAVMKK 120
                                                                                                                                                                                 181 LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
                                                                                                                                                                                                                     181 LLAAQEYAASQGLPAPRNVLIPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRI 240
                                                                                                                                                                                                                                                               241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300
                                                                                                                                                                                                                                                                                                                                         RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360
                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,267
FILING DATE: 08-UN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02528
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E:
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08454267
Patent No. 5843739
GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: STERNE, KESSLER, GOLDSTEIN & FOX, 1100 NEW YORK AVENUE, NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION: 12610
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       361 RSNPAKIVPAKSKNK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 RSSSARAARNRVKKE 374
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amino acid
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                                                                                                                   LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
                                                                                                                                                                                                FKGQPSVVHVHIKRHIMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300
IDWWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLIGWVLAQRCGCLSSSIAVMKK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3934
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,267
FILING DATE: 08-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-41,264
HER: 0623.0310000/JAG/GER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02528
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 0623.0310000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 374 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 374 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MOLECULE TYPE: protein US-08-454-267-2
                                                                                                                                                                                                                                                                                                                                                      361 RSNPAK 366
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Query Match 75.0%; Score 1450.5; DB 2; Length 374; Best Local Similarity 70.7%; Pred. No. 1.1e-150; Matches 265; Conservative 51; Mismatches 58; Indels 1;

Mon Jul 12 10:08:46 2004

191-00-260-5T6-60-80

g 셤  $\delta$ ò g  $\delta$ qq Š 쉱  $\delta$ 8 ò g 181 LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240 241 LKGQSSVIHVRMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTF-DEBIRPIG 299 241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300 61 IDWWAGVKVOIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAORSGCLGSTLAVMKK 120 SSKFLPVIGWSMWFSEXLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180 MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWL 60 1 MAIPLVLVVLPLGLLFLLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLAELLWLQLVWV 60 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE RESULT 4

US-09-941-319-2

Sequence 2, Application US/08941319

Sequence 2, Application US/08941319

Patent No. 294523

GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION:
DEPARTMENT OF INVENTION:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON NEW PORM:
NEDIUM TYPE: Ploppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,319
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
PREFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
TELEPHONE: (202) 371-2640
INFORMATION: POR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
TELEPHONE: 374 anino acids
TELEPHONE: 374 anino acids RSSSARAARNRVKKE 374 RSNPAKIVPAKSKNK 375 : 374 amino acids amino acids ; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-941-319-2 300 361 301 121 셤 d  $\stackrel{>}{\circ}$ 8 ద  $\delta$ 윱 ð à g à

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61 IDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK 120
                                                                                                                                                                                                                                                                                SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180
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                                                                                        1 MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWL
                                                                                                                     181 LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAJYDVTVAIPKSSPAPTMLRL
                                               1;
 Length 374;
                                               Indels
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; Sequence 6, Application US/08941319
; Patent No. 5945323
; GENERAL INFORMATION:
; APPLICANT: SLABAS, ANTONI R.
; APPLICANT: BROWN, ADRIAN P.
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
; NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,319
Query Match 75.0%; Score 1450.5; DB 2; Best Local Similarity 70.7%; Pred. No. 1.1e-150; Matches 265; Conservative 51; Mismatches 58;
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BER: 0623.0310000/JAG/GER
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,267
FILING DATE: 08-JUN-1995
APPLICATION NUMBER: PCT/GB93/02528
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 0623.031000C
TELECOMMUNICATION INFORMATION:
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US-08-941-319-6
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US-09-035-098-6
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                                                                                                                                        1 MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWL
                                                                                                                   Gaps
                                                                                                                 1;
                                                                                      Length 374;
                                                                                                                58; Indels
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Patent No. 6194640
GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.
                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                 ; Pred. No. 1.1e-150;
51; Mismatches 58;
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ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALURESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON
                                                                                   75.0%; Score 1450.5; 70.7%; Pred. No. 1.1e
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,267
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LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                265; Conservative
                                          protein
                              linear
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                                        TYPE:
                                              ; MOLECULE TO
US-08-941-319-6
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US-09-035-098-2
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                                                                                                                                                                                                             Length 374;
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Patent No. 6194640

GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           75.0%; Score 1450.5; DB 3; 70.7%; Pred. No. 1.1e-150; ive 51; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,098
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,267
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: P-41,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 RSNPAKIVPAKSKNK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 RSSSARAARNRVKKE 374
TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                       : 374 amino acids amino acid
                                                                                                                                                                                                         Query Match
Best Local Similarity 70.7
Matches 265, Conservative
                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
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US-09-215-252-5
; Sequence 5, Application US/09215252
; Patent No. 6300487
; Patent No. 6300487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: HOLLENBACK, David
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT PILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US/09/215,252
; CURRENT FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NOS: 42
; LUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIN Ver. 2.0
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                                                                                                                                                                                Length 374;
                                                                                                                                                                              Query Match 75.0%; Score 1450.5; DB 3; Length Best Local Similarity 70.7%; Pred. No. 1.1e-150; Matches 265; Conservative 51; Mismatches 58; Indels
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-035-098-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 RSNPAKIVPAKSKNK 375
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360 RSSARAARNRVKKE 374
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; ORGANISM: Maize
US-09-215-252-5
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61 IDWWAGVKVOIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAORSGCLGSTLAVMKK 120
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                                                                                                                                                   121 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180
                                                                                                                                                                               121 SSKFLPVIGWSMWFAEYLFLERSWAKDEKTLKWGLQRLKDFPRPFWLALFVEGTRFTPAK 180
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; Sequence 5, Application US/09970989A
; Patent No. 6670143
; GENERAL INFORMATION:
; APPLICANT: BOUNEL, DANIEL
APPLICANT: HOLLENBACK, DAVID
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; CURRENT APPLICATION NUMBER: US/09/970,989A
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 374
                                                                                                                                                                                                                                                         LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPALYDVTVAIPKSSPAPTMLRL
                                                                                                                                                                                                                                                                                                                                                            241 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG
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1 MAIPLVLVVLPLGLLFLLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLAELLWLQLVWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSNPAKIVPAKSKNK 375
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RSSSARAARNRVKKE 374
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CRGANISM: Zea mays
US-09-970-989A-5
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US-09-970-989A-5
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4 AAAVIVPLGILFFISGLVVNLL----
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                                                                                                                                                     361 RSNPAKIVPAKSKNK 375
                                                                                                                                                                                    RSSSARAARNRVKKE 374
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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US-08-454-267-7
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                                                   LKGQSSVIHVRMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTF.DEEIRPIG 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDWWAGVKVOIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180
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                                RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,581B

FILING DATE: March 14, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB96/00306

PILING DATE: 09-FEB-1996

APPLICATION NUMBER: GB 9502468.3

FILING DATE: 09-FEB-1995

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

STRANDEDNESS: single
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                                                                                                                                                                                                           Sequence 5, Application US/08818581B
Patent No. 6583340
GENERAL INFORMATION:
APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: BROWN, Adrian Paul
APPLICANT: BROWGH, Clare Louise
APPLICANT: KROON, Johannes Theodorus Maria
TITLE OF INVENTION: 2-ACYLTRANSFERASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
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                                                                                                                                                                                                                                                                                                                                                                  STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: US
                                                                                                                          RSSSARAARNRVKKE 374
                                                                                                 RSNPAKIVPAKSKNK 375
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Best Local Similarity 70.4<sup>3</sup>
Matches 264; Conservative
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ORIGINAL SOURCE:
ORGANISM: Zea mays
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241 FKGOPSVVHVHIKEHLMKELPDTDBAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPVIGWSMWFSEYLFLERNWAKDESTLKSGLQRLNDFPRPFWLALFVEGTRFTEAKLKAA 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
STATE: DC
COUNTRY: US
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION LATA:
APPLICATION NUMBER: US/08/454,267
FILING DATE: 08-JUN-1995
CLASSIFICATION NUMBER: PCT/GB93/02528
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
TELECOMMUNICATION INFORMATION:
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244
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                                                                                                                                                                                                                                                                  SLIVVISWACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNP 364
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                                                                                                                                 245 PSVVHVHIKRHIMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIK 304
                                                                                                                                                                                                                                                                                                    225 SLAVVLSWACLLTLGAMKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQSERSTP 284
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                                    QEYAASSELPVPRNVLIPRTKGFVSAVSNWRSFVPAIYDMTVAIPKTSPPPTMLRLFKGQ
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185 QEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFKGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-V8-19-1-19-7
Sequence 7, Application US/08941319
Fatent No. 594532
GENERAL INFORMATION:
FATEL CANT: BROWN, ADRIAN P.
TITLE OF INVENTION DIA BNCODING 2-ACVITRANSFERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
STATE: DC
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,319
FILING DATE: 08-JUN-1995
APPLICATION NUMBER: PCT(GB93/02528
FILING DATE: 08-JUN-1995
APPLICATION NUMBER: PCT(GB93/02528
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: RED, GRANT E.
REGESTRATION NUMBER: 623.0310000/JAG/GER
TELEFHONE: (202) 371-2500
INFORMATION POR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH PAPER: PCTOR: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: TELEFHONE: PCTOR: PCTOR: TELEFHONE: PCTOR: PCTOR: TELEFHONE: PCTOR: PCTOR: TELEFHONE: PCTOR: PCTOR: TELEFHONE: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR: PCTOR:
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AKVAPAKPKD 294
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64	WLIDWW	LLWLELV	INRVVAE	KSLYRR	YVVVRPVS	NLIQAIC	VVVPLGLLFPASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLIDWW	AVVVPLGLL	5 AAJ		ò
ч	Gaps	h 295; 79;	Length Indels	DB 3; e-118;	ore 1156.5; ed. No. 1.56 Mismatches	Score Pred. 33; Mis	% 4 % %	59.  larity 61.  Conservative	/ Match Local Similarity les 227; Conser	Query Match Best Local Matches 22	
			88 1	Ř Ω O	MG 2-ACYLTRANSFERASES GOLDSTEIN & FOX, P.L. WW, SUITE 600 5,098 67 67 4 3.0310000/JAG/GER	98 ING GOL E, N 35,0 35,0	ication US/09035098 40 TION: LABAS, ANTONI R. ROWN, ADRIAN P. INTION: DNA ENCODING UENCES: 7 E ADDRESS: STERNE, KESSLER, GOI OO NEW YORK AVENUE, P. INGTON IS STERNE: STERNE, COUPATIBLE IS POOR COMPATIBLE IS PATENTIN Release #1.0 CATION DATA: INUMBER: US/09/035,67 INUMBER: US/09/035,67 INUMBER: US/09/035,67 INUMBER: US/09/035,67 INUMBER: P-41,264 INUMBER: P-41,264 INUMBER: P-41,264 INUMBER: P-41,264 INUMBER: P-41,264 INUMBER: OS/33.71-2600 202) 371-2540 INUMBER: OS/33.71-2600 202) 371-2540 INUMBER: SEQ ID NO: 7: ACTERISTICS: Samino acids Innear Innear	of the principle of the control of t		Page 900 Pag	A D T T T T T T T T T T T T T T T T T T
284 4	ALSKES!	TTTKSST	LTLCMC	SALGLG	SSWKGLAL	HINNEL	LTLGAMK	SEAVVESWACELTEGAMKFERWSNEFSSWKGLAESALGEGTTTECMQTETKSSQSEKST	225 SLA		a a
364	SERSNP	LLIOFSC	VTALMO	SAFGLAV	SSWKGVAF	LOWSSLL 	VVAGSVKE	SLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNP			ò

PSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIK 304

105 QEYAASSELPVPRNVLIPRTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPPPTMLRLFKGQ 164

QEYATSTGLPVPRNVL1PRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFKGQ

185

B Q B ov

245 165

6

244

45 LPVIGWSMWFSEYLFLERNWAKDESTLKSGLQRLNDFPRPFWLALFVEGTRFTEAKLKAA 104

125 LPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAA

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124
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Sequence 13, Application US/09215252;
Parent No. 6300487;
GENERAL INFORMATION:
APPLICANT: LEUNG, David W.
APPLICANT: ADOUREL, Daniel
APPLICANT: HOLLENBACK, David
TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE;
FILE REFERENCE: 077319/0151;
CURRENT APPLICATION NUMBER: US/09/215,252
CURRENT FILING DATE: 1998-12-18;
PRIOR FILING DATE: 1996-03-19;
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                45 LPVIGWSMWFSEYLFLERNWAKDESTLKSGLQRLNDFPRPFWLALFVEGTRFTEAKLKAA
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                           4 AAAVIVPLGILFFISGLVVNLL--
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; ORGANISM: Homo sapiens
US-09-215-252-13
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US-09-215-252-13
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65 AGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKKSSKF 124
                                                                                                               LPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLLAA 184
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ZIP: 10036
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OSS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,581B
FILING DATE: March 14, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/00306
FILING DATE: 09-FEB-1995
FILING DATE: 09-FEB-1995
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TWATH: 311 amino acids
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US-08-818-581B-6
; Sequence 6, Application US/08818581B
; Patent No. 6583340
; Patent No. 6583340
; APPLICANT: SLABAS, Antoni Ryszard
; APPLICANT: BROWN, Adrian Paul
; APPLICANT: BROWN, Obhannes Theodorus Maria
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT
; TITLE OF INVENTION: 2-ACYLTRANSFERASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
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1185 Avenue of the Americas
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ORIGINAL SOURCE
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STREET: 118
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312 WACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTAL 349

Search completed: July 7, 2004, 13:42:25 Job time: 24 secs දුරු පු

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

(without alignments) 1805,431 Million cell updates/sec 7, 2004, 13:33:02 ; Search time 59 Seconds July Run on:

US-09-914-098-56 1935 1 MAIAAAVVVPLGLLFFASG......QSERSNPAKIVPAKSKNKGS 377 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2004s:\* 4.0.0 6.00 •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Co trading	ID	AAB08478	AAY99482	AAY99473	131	AAG13219	AAR99249	AAG51330	AAR59712	990	AAE15288	AAB08477	AAB08479	58	AAG51311	AAG13220	AAG33441	AAR59713	133	AAG51312	AAG13221	AAG33442	558	AAG51332	AAG33443	AAG31584
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## ALIGNMENTS

RESULT 1 AAB08478

Æ. AAB08478 standard; protein; 377

AAB08478; 

20-DEC-2000 (first entry)

Nucleotide sequence of a lysophosphatidic acid acetyltransferase.

Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant; triacylglycerol; oil content.

Glycine max.

WO200049156-A2.

24-AUG-2000.

22-FEB-2000; 2000WO-US004526.

99US-0121119P. 22-FEB-1999; (DUPO ) DU PONT DE NEMOURS & CO E I.

Ripp Kinney AJ, Hitz WD, Cahoon EB, Cahoon RE,

<u>Қ</u>

WPI; 2000-558300/51. N-PSDB; AAA64200.

New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal.

Claim 31; Page 99-100; 102pp; English.

The present sequence represents a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes

us-09-914-098-56.rag

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Local Matches

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The invention relates to nucleic acids encoding novel plant
acyltransferase-like proteins (AAA37343-A37445) which comprise one of 8
conserved acyltransferase motifs (AAY99474-Y99481). Acyltransferases
Catalyse the transfer of acyl groups from a donor to a variety of
substrates such as glycerides, sterols, stanols and phosphatides. Such
caralyse the transfer of acyl groups from a donor to a variety of
substrates such as glycerides, sterols, stanols and phosphatides. Such
characteristics of the plant. For example, cold-hardened plants have
different lipid concentrations in the cell membrane compared to non-
hardened plants, which makes the membrane more fluid and the plant more
can be used as probes or for expressing acyltransferase-like proteins in
host cells e.g., for recombinant protein production. They may be
expressed in plant cells to alter the lipid composition of the plant
e.g., for the production of chill-resistant plants, or for altering the
composition of plant oils. The present sequence represents jojoba
lysophosphatidic acid acyltransferase (LPAAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKLGLQRLKDYPLPFWLALFVEGTRFTQAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lysophosphatidic acid acyltransferase, ATLPAAT1, lipid synthesis, recombinant expression, membrane fluidity, cold resistance,
                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 387;
                                                                                                                                                                                                                                                                                                                                                                         83.2%; Score 1609.5; DB 3; Length 81.3%; Pred. No. 6.5e-160; ive 29; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana acyltransferase ATLPAAT1.
       5; Page 98-99; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein; 389 AA.
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                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 81.3
Matches 304; Conservative
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                                                                                                                                                                                                                                                                                                                                         Sequence 387 AA;
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                                                                                                      1 MAIAAAAVVVPLGILFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lysophosphatidic acid acyltransferase; LPAAT; jojoba; lipid synthesis; recombinant expression; membrane fluidity; cold resistance;
                                                                          Gaps
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0
                                      Length 377;
                                                                       Indels
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                                     DB 3;
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                                                      4e-194;
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                                                     Pred. No. 4e-
Mismatches
                                     Score 1935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY99482 standard; protein; 387 AA
                                  100.0%; Sc
100.0%; Pr
tive 0;
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                                                                      Conservative
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                                                al Similarity
377; Conserv
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N-PSDB; AAA37472.
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Sequence 377
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                                 Query Match
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AAY99482;

RESULT 2
AAY99482
ID AAY9
XX
AC AAY9
XX
DT 15-A
XX
DE JOJO
XX
XX
COS SIMT
XX
COS SIMT
XX
PT Misc
FT Misc
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PN WO2C
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PN WO2C
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120 119 180 179 240

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Gaps

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300

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The invention relates to nucleic acids encoding novel plant

CC acyltransferase-like proteins (AAA37343-A37445) which comprise one of 8

CC conserved acyltransferase motifs (AAY99474-Y99481). Acyltransferases

CC catalyse the transfer of acyl groups from a donor to a variety of

CC substrates such as glycerides, sterols, stanols and phosphatides. Such

CC characteristics of the plant. For example, cold-hardened plants have

CC different lipid concentrations in the cell membrane compared to non-

CC different lipid concentrations in the cell membrane and the plant more

CC different lipid concentrations in the cell membrane of the plant wore

CC different lipid concentrations in the cell membrane for acid sequences of the invention

CC colerant of low temperatures. The nucleic acid sequences of the invention

CC can be used as probes or for expressing acyltransferase-like proteins in

CC can be used as probes or for expressing acyltransferase-like proteins in

CC composition of plant cells to alter the lipid composition of the plant

CC composition of plant oils. Sequences AAY99463-Y99473 represent cDNAs

CC and lysophosphatidic acid acyltransferases ATATI-ATAT4, ATAT6-ATAT11
                                                                                                                                                                                                                                                                Novel acyltransferase related proteins useful for altering membrane fluidity in plant cells e.g. to induce chill tolerance.
                                                                                                                                                                                                                                                                                                                                      Example 5; Page 75-76; 126pp; English
                                                                                                                                                                                                   WPI; 2000-303447/26.
                                                                                                            (CALJ ) CALGENE LLC
                                                                                                                                                                                                                            N-PSDB; AAA37342
                                                              25-SEP-1998;
                    24-SEP-1999;
                                                                                                                                                         Lassner MW,
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(first entry)

18-OCT-2000

Van Eenennaam A;

Ruezinsky DM,

Emig RA,

99WO-US022231 98US-0101939P

AAG51310;

GOPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRP 302 122 KFLDVIGWSMWFSEYLFLERNWAKDESTLKSGLQRLSDFPRPFWLALFVEGTRFTEAKLK 181 3 IAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLID 62 WWAGVKVOIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAORSGCLGSTLAVMKKSS KFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLL AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFK 182 AAQEYAASSELPIPRNVLIPRTKGFVSAVSNMRSFVPAIYDMTVTIPKTSPPPTMLRLFK 0; Gaps Query Match
Best Local Similarity 77.2%; Pred. No. 9.2e-156;
Matches 287; Conservative 43; Mismatches 42; Indels 363 NPAKIVPAKSKN 374 Sequence 389 AA; 123 183 243 242 63 62 Db 8  $\dot{\delta}$  $\delta$ g δ

242

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303 IKSLLVVISWACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSFRS 362 |||:|||| |: 362 TPAKVVPAKPKD 373 g 임 ò

AAG51310 standard; protein; 389 AA. RESULT 4 AAG51310 ID AAG5

99US-0139459P. 99US-0139460P. 99US-0139461P.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. Arabidopsis thaliana protein fragment SEQ ID NO: 65110. 99US-0137528P. 99US-0137502P. 99US-0137724P. 99US-0138094P. 99US-0138840P. 99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-012628234P.
99US-0128234P.
99US-013077P.
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99US-0132488P. 99US-0134370P. 99US-0134768P. 99US-0134941P. 99US-0135124P. 99US-0135353P. 990S-0139119P. 990S-0139452P. 990S-0139453P. 990S-0139454P. 990S-0139454P. 99US-0134218P. 99US-0134219P. 99US-0134221P. 99US-0136782P. 99US-0137222P. 99US-0136021P 25-FEB-2000; 2000EP-00301439 Arabidopsis thaliana. 14-MAY-1999; 18-MAY-1999; 19-MAY-1999; 20-MAY-1999; 04-MAY-1999; 05-MAY-1999; 06-MAY-1999; 06-MAY-1999; 07-MAY-1999; 25-MAR-1999; 29-MAR-1999; 01-APR-1999; 06-APR-1999; 08-APR-1999; 16-APR-1999; EP1033405-A2 06-SEP-2000 

PR 25-AUG-1999; 99US-0150566P. PR 26-AUG-1999; 99US-0150884P.	27-AUG-1999; 99US-015106 27-AUG-1999; 99US-015106	2/~AUG-1999; 99US-015108 30-AUG-1999; 99US-015130	31-AUG-1999; 99US-015143 01-SEP-1999; 99US-015193	07-SEP-1999; 99US-015236	10-SEP-1999; 99US-015307 13-SEP-1999; 99HS-015375	15-SEP-1999; 99US-015401	16-SEP-1999; 99US-015403;	22-SEP-1999; 99US-015513	23-SEP-1999; 99US-015548	28-SEP-1999; 99US-015565; 28-SEP-1999; 99US-015645	29-SEP-1999; 99US-015659	04-OCT-1999; 99US-015711;	06-OCT-1999; 99US-015786	07-OCT-1999; 99US-0158023	12-OCT-1999; 99US-015823; 12-OCT-1999; 99US-0158369	13-OCT-1999; 99US-0159293	13-OCT-1999; 99US-0159294	14-OCT-1999; 99US-0159325	14-OCT-1999; 99US-015933C	14-OCT-1999; 99US-0159331 14-OCT-1000: 00HS-0150637	14-OCT-1999; 99US-0159638	18-OCT-1999; 99US-0159584	Z1-OCT-1999; 99US-0160741 Z1-OCT-1999; 99US-0160767	21-OCT-1999; 99US-0160768	21-OCT-1999; 99US-0160770	21-OCT-1999; 99US-0160815	22-OCT-1999; 99US-0160980	22-OCT-1999; 99US-0160989	25-OCT-1999; 99US-0161404	ZS-OCT-1999; 990S-016140S 25-OCT-1999; 99DS-0161406	26-OCT-1999; 99US-0161359	26-OCT-1999; 99US-0161360 26-OCT-1999; 99US-0161361	28-OCT-1999; 99US-0161920	28-OCT-1999; 99US-0161992	29-OCT-1999; 99US-0162142	Match Match Control 18 10 10 10 10 10 10 10 10 10 10 10 10 10	com al Similarity 77.2%; Pred. No. 9.2e-156	tches 287; Conservative 43; Mismatches 4	OV 3 IAAAAVVVPIGII.FFASGII.VMI.TOATOVAAADDVSKSTVPPIGII.		LFFI SGLAVNLFQAVCYVL I RPLSKNT	QY 63 WWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTI		IDWLVGW	EYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVE			OY 183 AAQEYATSTGLPVPRNVLIPRTKGFVSAVSHWRSFVPAIYDVTVAIPKSSPAF
99US-0139462P. 99US-0139463P.	99US-0139763P.	99US-0139899P.	99US-0140354P.	99US-0140695P.	99US-0140991P.	99US-0141287P.	99US-0142154P.	99US-0142055P.	99US-0142803P.	99US-0142920P.	99US-0142977P.	99US-0143624P.	99US-0144005P.	99US-0144085F.	99US-0144325P.	99US-0144331P.	99US-0144333P.	99US-0144334P.	99US-0144355P.	99US-0144632P.	99US-0144884P.	99US-0145086P.	99US-0145088P.	99US-0145085P. 99US-0145087P	99US-0145089P.	99US-0145192P.	99US-0145218P.	99US-0145224P.	99US-0145913P.	99US-0145918P.	99US-0145919P. 99US-0145951P	99US-0146386P.	99US-0146388P.	99US-0147038P.	99US-0147204P.	99US-0147192P.	99US-0147260P.	99US-014/3U3F.	99US-0147493P.	99US-0147935P. 99US-0148171P	99US-0148319F.	99US-0148341P. 99US-0148565P	99US-0148684P,	99US-0149368P.	99US-0149175P. 99HS-0149426P	99US-0149722P.	99US-0149723P.	99US-0149902P.
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               GQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRP 302
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                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                           242 GQPSVVHVHIKCHSMKDLPESDDAIAQWCRDQFVAKDALLDKHIAADTFPGQQEQNIGRP
                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 12633.
                                                                                                                                                                                                AAG13219 standard; protein; 389 AA
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                                        242 GQPSVVHVHIKCHSMKDLPESDDAIAQWCRDQFVAKDALLDKHIAADTFPGQQEQNIGRP
                        3 IAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLID
                                                                                          WWAGVKIQVFADNETFNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKKSS
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
64-MAY-1999;
05-MAY-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
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30-JUN-1999;
01-JUL-1999;
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06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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18-MAY-1999;
19-MAY-1999;
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27-MAY-1999;
28-MAY-1999;
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18-JUN-1999;
18-JUN-1999;
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14-MAY-1999,
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                                                                                                                                                                                                                                                                                                                                                         FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300
                                                                                                                                                                                                                                                                                                                                                                                                 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360
                                        The amino acid sequence (AAR99249) was deduced of Limnanthes clone 1 (AAT35205), a cDNA clone obtd. by heterologous screening of a Limnanthes douglasii seed cDNA library using a 600 bp Ncol/PstI fragment of a rape 2-acyltransferase (2AT) clone corresponding to the N-terminus of the rape protein. Another isolated clone (AAT35204) codes for Limnanthes 2AT (AAR99248), which can be used to increase the erucic acid content of transgenic plants
                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                     MAIAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVABLLMLBLVWL
                                                                                                                                                                                                                                           LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL
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0
                                                                                                                                              77.7%; Score 1504; DB 2; Length 377; 76.2%; Pred. No. 7.5e-149; iive 45; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 65137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG51330 standard; protein; 360
                      Example 2; Fig 1; 54pp; English
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99US-0123180P.
99US-0123548P.
99US-0125788P.
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                                                                                                                                            Query Match
Best Local Similarity 76.2
Matches 279; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RSNPAK 366
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 improved oil prodn.
                                                                                                                           Sequence 377 AA;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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362
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                                                                                                                                                                                                                                                                                                                                                                                                                                 KFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAKLL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                             122 KFLPVIGWSMWFSEYLFLERNWAKDESTLKSGLQRLSDFPRPFWLALFVEGTRFTEAKLK 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 -----VVLSWACVLTLGAIKFLHWAQLFSSWKGITISALGLGIITLCMQILIRSSQSERS 332
                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                  303 IKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERS
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                           / Match 75.1%; Score 1453.5; DB 3; Length 360; Local Similarity 72.0%; Pred. No. 1.4e-143; Local Sonservative 40; Mismatches 35; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR59712 standard; protein; 374 AA.
        99US-0158369P.
99US-0159294P.
99US-0159294P.
99US-0159239P.
99US-01593310P.
99US-01593310P.
99US-0159638P.
99US-0159638P.
99US-0160741P.
99US-0160741P.
99US-0160741P.
99US-0160741P.
99US-0160741P.
99US-0160741P.
99US-0160741P.
99US-0160741P.
99US-0160741P.
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990S-0161920P.
990S-0161992P.
990S-0161993P.
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(first entry)
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        12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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26-JAN-1995
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Matches
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Complementation studies using a maize cDNA library transferred into E. coli UC201 allowed the isolation of a plasmid encoding a 2-acyltransferase enzyme from maize. DNA encoding 2-acyltransferase can be used to produce transgenic plants having altered lipid contents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct a plant 2-acryl-transferase - used to produce plants with decreased lipid levels and with a tailored lipid compsn. coli, transgenic plant; Escherichia 2-Acyltransferase; lipid; oilseed; English (NICK-) NICKERSON BIOCHEM LTD 92GB-00025845, Disclosure; Fig 1; 45pp; Maize 2-acyltransferase Brown AP; WPI; 1994-217888/26. N-PSDB; AAQ68267. crop improvement Sequence 374 AA; DNA encoding increased or WO9413814-A1 10-DEC-1993; 10-DEC-1992; 23-JUN-1994 AR, Slabas Zea DNA 

7 Gaps ; 75.1%; Score 1453.5; DB 2; Length 374; 70.9%; Pred. No. 1.5e-143; ive 50; Mismatches 58; Indels 1; Conservative Query Match Best Local Similarity Matches 266; Conserv

240 240 300 299 360 359 120 180 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK 180 IDWWAGVKVOIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAORSGCLGSTLAVMKK 120 9 9 241 LKGQSSVIHVRMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 301 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE LLAAQEYATSTGL PVPRNVLI PRTKGFVSAVSHMRSFVPAIYDVTVAI PKSSPAPTMLRL FKGQPSVVHVHIKRHIMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLBLVWL RSNPAKIVPAKSKNK 375 181 241 361 Н 61 121 121 181 61 Dp ద  $\delta$ д · & 셤 ò 원 吕 ð ò ઠ

AAU00667 standard; protein; 374 RESULT 9
AAU00667
ID AAU0
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360

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(first entry) 07-SEP-2001 

Maize lysophosphatidic acid acyltransferase (LPAAT)

Lysophosphatidic acid acyltransferase epsilon; LPAAT-epsilon; LPA; PA; lysophosphatidic acid; phosphatidic acid; acylation; cellular activation; phospholipid signalling; mitogenesis; inflammation; autoimmune disease; oncology; cancer; obesity; gene therapy; maize.

Zea

WO200134782-A1

17-MAY-2001

02-NOV-2000; 2000WO-US030193

99US-00436919 09-NOV-1999; (CELL-) CELL THERAPEUTICS INC

DW; Leung WPI; 2001-335920/35.

Novel isolated human isoform of lysophosphatidic acid acyltransferase-epsilon useful for diagnostic, therapeutic and screening purposes.

Example 1; Fig 2; 48pp; English.

The sequence represents a maize lysophosphatidic acid acyltransferase (LPAAT) isoform, LPAAT-delta, similar to a human LPAAT isoform, LPAAT
C (PAAT) isoform, LPAAT-delta, similar to a human LPAAT isoform, LPAAT
C (PSI)on. LPAAT catalyses the acylation of lysophosphatidic acid (LPA) to phosphatidic acid (PA). LPA and PA have been identified as phospholipid signalling molecules that affect a wide range of biological responses. PA is involved in cellular activation and mitogenesis. Compounds that block PA generation and hence diminish lipid biosynthesis and the signal involved in cell activation are of therapeutic interest in the areas of inflammation and oncology (e.g. autoimmune diseases and cancer) as well continity of LPAAT-epsilon and its corresponding DNA can be used activity of LPAAT and, therefore, PA. The DNA is useful in tests to detect the presence or expression of LPAAT-epsilon in relation to certain diseases and conditions, and in disease prevention and treatment. The sequences of the invention are also useful for diagnosis of diseases and conditions in which the expression of LPAAT enzyme is abnormal

Sequence 374 AA;

Gaps .. Score 1450.5; DB 4; Length 374; Pred. No. 3.1e-143; 1; Mismatches 58; Indels 1; 75.0%; Scc 70.7%; Pre tive 51; Query Match Best Local Similarity 70.7' Matches 265; Conservative

120 180 61 IDWWAGVKYQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIORLSDFPLPFWLALFVEGTRFTQAK 121 g

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180 240 181 LLAAQEYAASQGLPAPRNVLIPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRI LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 181 g ò  $\delta$ 

300 FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 

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61 VDWWAGVKVQLHADEETYRSMGKEHALIISNHRSDIDWLIGWILAQRSGCLGSTLAVMKK 120
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                                                                      241 LKGQSSVIHVRMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to polypeptides with lysophosphatidic acid acyltransferase (LPAT) activity and polynucleotides encoding such polypeptides. LPAAT also referred as 1-acyl sn-glycerol-3- phosphate acyltransferase (EC 2.3.1.51), catalyses the acylation of lysophosphatidic acid (LPA) to phosphatidic acid (PA). Polypeptides of the invention are used for identifying specific modulators, potentially useful for regulating cellular pathways, e.g. to augment trilineage haematopolesis after cytoreductive therapy or to inhibit inflammation after hypoxia and reoxygenation injury (e.g. sepsis, trauma and adult respiratory distress syndrome). The present sequence is maize LPAAT
                                           RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding human lysophosphatidic acid acyltransferase, useful for identifying specific inhibitors, e.g. for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lysophosphatidic acid acyltransferase; LPAAT protein; trauma; 1-acyl sn-glycerol-3-phosphate acyltransferase; reoxygenation injury; cellular pathway regulation; trilineage haematopoiesis; inflammation; cytoreductive therapy; adult respiratory distress syndrome; hypoxia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 374;
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                                                                                                                                                                                                                                                                                                    AAE15288 standard; protein; 374 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CELL-) CELL THERAPEUTICS INC
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                                                                                                                                       RSNPAKI VPAKSKNK 375
                                                                                                                                                                               360 RSSSARAARNRVKKE 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize LPAAT protein.
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es 265; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis; maize
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                                                                                                                                                                                                                                                      RESULT 10
AAE15288
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61 IDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK 120

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1 MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLMLELVWL

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The present sequence represents a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal.
121 SSKFLPVIGWSMWFAEYLFLERSWAKDEKTLKWGLQRLKDFPRPFWLALFVEGTRFTPAK
                                                                                                                                                   241 LKGQSSVIHVRMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG
                                                                                                                                                                                                    301 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE
                                                                                                                                                                                                                          LLAAQEYAASQGLPAPRNVLIPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRI
                                                                                                                           241 FKGQPSVVHVHIKRHIMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG
                                                 LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant; triacylglycerol; oil content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a lysophosphatidic acid acetyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAB08477 standard; protein; 374 AA.
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                                                                                                                                                                                                                                                                                RSNPAKIVPAKSKNK 375
                                                                                                                                                                                                                                                                                                                     360 RSSSARAARNRVKKE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0121119P
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Gaps 1; Length 374; Indels 3; ; Score 1431.5; DB 3; ; Pred. No. 3.1e-141; 47; Mismatches 55; 74.08; 71.98; Similarity 71.9 263; Local Query Mat Best Loca Matches

Ή, 240 300 120 LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPALYDVTVAIPKSSPAPTMLRL 240 9 9 SSKFLPVIGWSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLMLELVWL IDWWAGVKVQIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSTLAVMKK RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE RSNPAK 366 RSSSAK 365 121 241 300 360 61 61 121 181 181 301 361 g d Q Db ò d  $\delta$  $\overset{\circ}{\circ}$ 셤 ò  $\delta$ 8

AAB08479 standard; protein; 374 AAB08479

AAB08479;

(first entry) 20-DEC-2000 Amino acid sequence of a lysophosphatidic acid acetyltransferase.

Lysophosphatidic acid acetyltransferase, LPAAT; transgenic plant, triacylglycerol; oil content.

Triticum aestivum.

WO200049156-A2

22-FEB-2000; 2000WO-US004526

99US-0121119P 22-FEB-1999;

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PONT DE NEMOURS &

UD ( DANG)

Ripp AJ, Kinney WD, Hitz Cahoon RE, Cahoon EB,

2000-558300/51. WPI; 2000-558300/9 N-PSDB; AAA64201.

New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal.

31; Page 101-102; 102pp; English Claim

The present sequence represents a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. 

This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes 5555555X8

Sequence 374 AA

240 360 180 240 300 299 120 120 180 60 SSKFLPVIGWSMWFAEYLFLERSWAKDEKTLKSGLQRLKDFPRSFWLALFVEGTRFTPAK LLAAQEYATSTGLPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL FKGQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG SSKFLPVIGWSMWFSEXLFLERSWAKDESTLKSGIQRLSDFPLPFWLALFVEGTRFTQAK LLAAQEYAVSQGLTAPRNVLIPRTKGFVSAVSIMRDFVPAIYDTTVIIPEDSPRPTMLRI RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 1 MAIAAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLELVWL IDWWAGVKVOIFTDHETFRLMGKEHALVISNHRSDIDWLVGWVSAORSGCLGSTLAVMKK Gaps 1; Length 374; 53; Indels ω ,, Score 1414.5; DB 3; Pred. No. 1.9e-139; 2; Mismatches 53; 73.1%; Sco llarity 71.0%; Pre Conservative 52; RSNPAK 366 ||: || RSSSAK 365 Similarity Best Local Sim Matches 260; 121 181 241 301 300 361 360 н 61 181 241 121 61 Query Match g Q a ď  $\delta$ 원  $\delta$ 8 8  $\delta$ g &  $\delta$ 

Ė AAG31583 standard; protein; 376

AAG31583;

17-OCT-2000

pathway; on; signal transduction pathway; metabolic genetic mapping; gene expression control; Protein identification; hybridisation assay; termination sequence.

Arabidopsis thaliana protein fragment SEQ ID NO: 37953

Arabidopsis thaliana

EP1033405-A2

06-SEP-2000

2000EP-00301439 25-FEB-2000;

99US-0121825P. 99US-0123180P. 99US-0123548P. 99US-0125788P. 99US-0126264P. 99US-0126785P. 99US-0127462P. 25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; AAG31583
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         Arabidopsis thaliana.
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                                                                                                                                                                                                            66.0%; Score 1277; DB 3; 62.3%; Pred. No. 5.2e-125; ive 62; Mismatches 76;
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29-JUN-1999; 30-JUN-1999; 01-JUL-1999; 02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 13-JUL-1999; 13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999;

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PESDDAIAQWCRDQFVAKDALLDKHIAADTFPGQOEQNIGRPIKSLAVVLSWACVLTLGA
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99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0155139P.
99US-015568P.
99US-0156458P.
99US-015658P.
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12-AUG-1999; 13-AUG-1999;

18-AUG-1999; 20-AUG-1999; 20-AUG-1999;

20-AUG-1999; 23-AUG-1999; 23-AUG-1999;

25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999;

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Query Match 64.1%; Score 1240; DB 3; Length 310; Best Local Similarity 78.2%; Pred. No. 3e-121; Matches 230; Conservative 30; Mismatches 34; Indels 0;
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